

863046

**STIC-Biotech/ChemLib**

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**From:** Bunner, Bridget  
**Sent:** Thursday, January 23, 2003 2:33 PM  
**To:** STIC-Biotech/ChemLib  
**Subject:** sequence search

Hi! I'd like a sequence search performed for case 09/893,348:

1. the amino acid sequence of SEQ ID NO: 19

Thanks!

Bridget Bunner

Art Unit 1647  
CM1-10D12  
(703) 305-7148  
mailbox 10B19

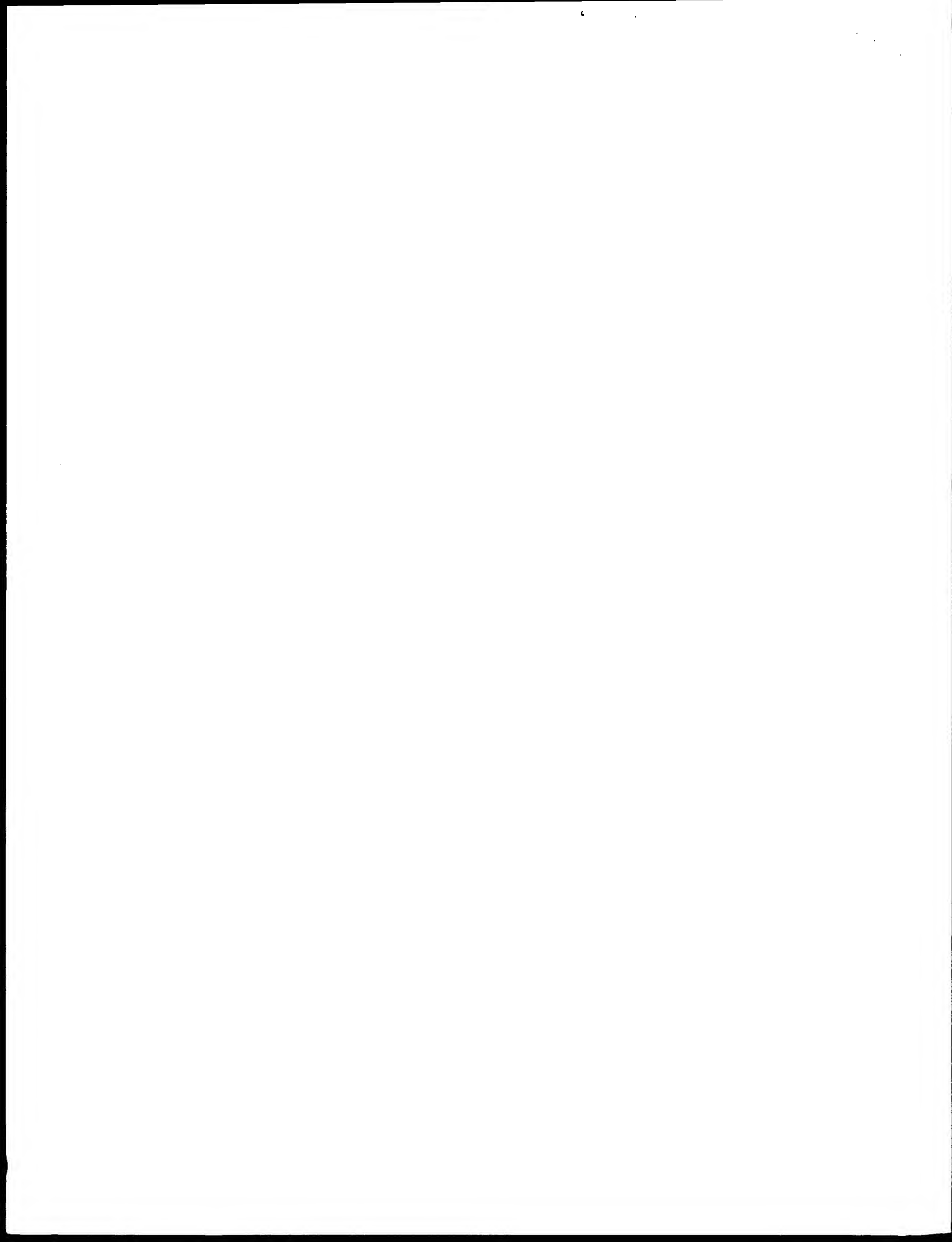
CONF

POINT OF CONTACT  
PAUL SCHULWITZ  
TECHNICAL INFO. SPECIALIST  
LABOR TEL (703) 305-1954

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 1/24  
Date Completed: 1/24  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



GenCore version 5.1.3  
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protein - protein search, using sw model

January 24, 2003, 11:08:03 ; Search time 35 Seconds  
(without alignments)  
68.529 Million cell updates/sec

US-09-893-348-19

1 SYDSIKLEPPPPPEFA 18

BLOSUM62

Gapop 10 0 , Gapext 0 5

908470 seqs, 133250620 residues

total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Minimum PR seq length: 2000000000

str-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

tabase :

A\_Geneseq\_101002:\*

1: /SID27/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*

2: /SID27/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SID27/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*

4: /SID27/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*

5: /SID27/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*

6: /SID27/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*

7: /SID27/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SID27/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SID27/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SID27/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*

11: /SID27/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SID27/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SID27/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SID27/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SID27/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SID27/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SID27/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SID27/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SID27/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*

20: /SID27/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*

21: /SID27/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SID27/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

23: /SID27/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	18	21	AAV71335
2	99	100.0	181	21	AAV71400
3	99	100.0	356	21	AAV71390
4	99	100.0	374	21	AAV71397
5	99	100.0	475	21	AAV71389
6	99	100.0	502	21	AAV71396
7	99	100.0	552	21	AAV71388
8	99	100.0	684	21	AAV71394
9	99	100.0	695	21	AAV71387
10	99	100.0	732	21	AAV71399

11	99	100.0	736	21	AAV71398	Rat Nogo A protein
12	99	100.0	737	21	AAV71386	Rat Nogo A protein
13	99	100.0	746	21	AAV71391	Rat Nogo A protein
14	99	100.0	803	21	AAV71562	Rat Nogo A protein
15	99	100.0	974	21	AAV71560	Rat Nogo A protein
16	99	100.0	1162	21	AAV71557	Rat Nogo A protein
17	99	100.0	1163	21	AAV71310	Rat neurite growth
18	99	100.0	1163	21	AAV71384	Alternative versio
19	85	85.9	642	19	AAW58383	Human secreted pro
20	85	85.9	642	22	AAB90682	Human Rg160_1 prot
21	85	85.9	893	21	AAV95012	Human secreted pro
22	85	85.9	1178	21	AAV71311	Human neurite grow
23	85	85.9	1192	21	AAV56967	Human MAG1 polypep
24	85	85.9	1192	22	AAU04591	Human Nogo protein
25	85	85.9	1192	22	AAB82349	Human Nogo-A prote
26	85	85.9	1246	22	AAU33228	Novel human secret
27	50	50.5	182	13	AAP26502	Guayule rpp. Part
28	50	50.5	473	16	AAR75177	Guayule rubber par
29	50	50.5	473	18	AAW23567	Guayule rubber par
30	50	50.5	473	19	AAW53236	Guayule rubber par
31	50	50.5	473	21	AAE28241	Guayule rubber par
32	49	49.5	306	22	ABR65928	Guayule rubber par
33	48	48.5	58	23	ABP11344	Human ORFX protein
34	48	48.5	104	23	ABR04515	Murine apoptosis r
35	47	47.5	58	22	AAE80869	Lipid biosynthesis
36	47	47.5	58	22	AAE83316	Arabidopsis thalia
37	46	46.5	93	21	AAE34620	Arabidopsis thalia
38	46	46.5	164	21	AAE46235	Arabidopsis thalia
39	46	46.5	168	21	AAE34619	Arabidopsis thalia
40	46	46.5	187	21	AAE46234	Arabidopsis thalia
41	46	46.5	227	21	AAE46233	Arabidopsis thalia
42	46	46.5	275	21	AAE46209	Arabidopsis thalia
43	46	46.5	340	21	AAE46208	Arabidopsis thalia
44	46	46.5	340	23	ABE93394	Herbicidally activ
45	46	46.5	355	21	AAE46207	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AAV71335	standard; peptide; 18 AA.
ID	AAV71335	
AC	AAV71335;	
DT	02-NOV-2000	(first entry)
DE	Bovine P472 peptide for antisera production	
XX		
KW	Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;	
KW	central nervous system; neoplastic disease; antiproliferative; glioma;	
KW	antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;	
KW	degenerative nerve disease; Alzheimer's disease; Parkinson's disease;	
KW	hyperproliferative disorder; benign dysproliferative disorder; diagnosis;	
KW	psoriasis; tissue hypertrophy; neuronal regeneration; treatment;	
KW	structural plasticity; screening; P472 peptide; AS 472; antiserum.	
OS	Bos sp.	
XX		
PN	WO2000031235-A2.	
PD	02-JUN-2000.	
XX		
PF	05-NOV-1999;	99WO-US26160.
XX		
PR	06-NOV-1998;	98US-0107446.
XX		
PA	(SCHW/) SCHWAB M E.	
XX	(CHEN/) CHEN M S.	
PI	Schwab ME, Chen MS;	

WPI; 2000 400052/34.

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons

Claim 22; Page 59; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a bovine peptide P472 used for antisense fragment corresponding to residues 623-640 with three mismatches. Note: The present sequence is designated as SEQ ID NO. 33 in the specification. However, in claim 22, SEQ ID NO. 33 is referred as being nucleic acid sequence SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 18 AA;

Query Match 100.0%; Score 99; DP 21; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1,3e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SYDSIKLEPENPPPYEEA 18  
1 SYDSIKLEPENPPPYEEA 18

RESULT 2

AAV71400 standard; Protein; 181 AA

AAV71400;

02 NOV 2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant NiG-D20.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutain; mutuin.

Ratius sp.

W0200031235 A2.

02 NOV 2000.

05 NOV 1999; 09W0 0506160

06 NOV 1998; 0808 0107446.

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX PI Schwab ME, Chen MS;

XX WPI; 2000-400052/34

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page , 122pp, English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NiG-D20. NiG-D20 is composed of His-tag/T7 tag/Nogo A sequence aa 542-722/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo A protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 181 AA;

Query Match 100.0%; Score 99; DP 21; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1,3e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSIKLEPENPPPYEEA 18  
Db 82 SYDSIKLEPENPPPYEEA 99

RESULT 3

AAV71390 standard; Protein; 356 AA.

AAV71390;

02 NOV 2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant NiG-D20.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutain; mutuin.

Rattus sp.

WO200031235-A2.

02-JUN-2000.

05-NOV-1998; 98US-0107446.

06-NOV-1998; 98US-0107446.

(SCHW/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000-400052/34.

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page : 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant NiG-D5. NiG-D5 is composed of His-tag/T7-tag/Nogo-A sequence aa 291-646/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 356 AA;

Query Match 100.0%; Score 99; DB 21; Length 356;  
Best Local Similarity 100.0%; Pred No 2.7e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYDSIKLEPENPPPYEEA 18  
|||||  
333 SYDSIKLEPENPPPYEEA 350

SUULT 4

AAY71397 standard; Protein; 374 AA.

AAY71397;

02 NOV-2000 (first entry)

DE Rat Nogo A protein fragment used in the construction of mutant NiG-D16.  
XX  
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.  
XX  
OS Rattus sp.  
XX  
XX  
FH Key Location/Qualifiers  
FT Region 1..18 /note= "Corresponds to residues 172-189 of Nogo A  
FT sequence shown in AAY71310"  
FT 19..374  
FT Region /note= "Corresponds to residues 619-974 of Nogo A  
FT sequence shown in AAY71310"  
XX  
XX  
PN WO200031235 A2.  
XX  
PD 02-JUN-2000.  
XX  
XX 05-NOV-1998; 99WO-US26160.  
XX 06-NOV-1998; 98US-0107446.  
XX  
XX (SCHW/) SCHWAB M E.  
XX (CHEN/) CHEN M S.  
XX  
XX Schwab ME, Chen MS;  
XX WPI; 2000-400052/34.  
XX  
XX Nogo proteins and nucleic acids useful for treating neoplastic  
PT disorders of the central nervous system and inducing regeneration of  
PT neurons -  
XX  
XX  
PS Example; Page : 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is natively associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAY71310, which is used in the construction of mutant NiG-D16. NiG-D16 is composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 619-974/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.





growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutic which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of the A protein shown in AAY71310, which is used in the construction of mutant NiG-D15. NiG-D15 is composed of His-tag/T7-tag/Nogo-A sequence aa 172-189 + 491-974/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 502 AA;  
Query Match 100.0%; Score 99; DB 21; Length 502;  
Best Local Similarity 100.0%; Pred. No. 4e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYDSIKLEPENPPYEAA 18  
151 SYDSIKLEPENPPYEAA 168

ULT 7  
71388  
AAY71388 standard; Protein; 552 AA.

AAY71388;

02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant NiG-D3.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.

Rattus sp.

WO200031235 A2.

02-JUN-2000.

05-NOV-1999; 7377-3526160.

06-NOV-1998; 98US-0107446.

(SCHW/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS,

DP WPI; 2000-400052/34.  
XX Nogo proteins and nucleic acids useful for treating neoplastic  
PT disorders of the central nervous system and inducing regeneration of  
PT neurons -  
XX Example; Page -; 122pp; English.

XX The patent relates to neurite growth inhibitor Nogo which is free of  
CC all central nervous system (CNS) myelin material with which it is  
CC natively associated. Nogo proteins and fragments displaying neurite  
CC growth inhibitory activity are used in the treatment of neoplastic  
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,  
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic  
CC neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma  
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's  
CC diseases. Therapeutics which promote Nogo activity can be used to treat  
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.  
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic  
CC acids can be used to inhibit production of Nogo protein to induce  
CC regeneration of neurons or to promote structural plasticity of the CNS  
CC in disorders where neurite growth, regeneration or maintenance are  
CC deficient or desired. The animal models can be used in diagnostic and  
CC screening methods for predisposition to disorders and to screen for or  
CC test molecules which can treat or prevent disorders or diseases of the  
CC CNS. The present sequence is a fragment of rat Nogo A protein shown in  
CC AAY71310, which is used in the construction of mutant NiG-D3. NiG-D3  
CC is composed of His-tag/T7-tag/Nogo-A sequence aa 172-723/His-tag.  
CC Nogo A deletion mutants were used for mapping the inhibitory sites of  
CC Nogo protein. Major inhibitory region was identified in the  
CC Nogo A sequence from amino acids 172-974, particularly amino acids  
CC 542-722. In addition, N-terminal region 1-171 was found to be inhibitory  
CC to NIH 3T3 fibroblast spreading.  
CC Note: The present sequence is not given in the specification but is  
CC derived from rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42  
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However, the specification does not include sequences for  
CC these SEQ ID numbers.

Sequence 552 AA;

Query Match 100.0%; Score 99; DB 21; Length 552;  
Best Local Similarity 100.0%; Pred. No. 4.4e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSIKLEPENPPYEAA 18  
Nb 452 SYDSIKLEPENPPYEAA 469

RESULT 8  
AAY71394  
ID AAY71394 standard; Protein; 684 AA.

XX AAY71394;

02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant NiG-D10.

Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.

Rattus sp.

WO200031235-A2.

02-JUN-2000.

05 NOV 1999 09:00:00  
06 NOV 1999 09:05:0107446

(SCHW/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS;  
WPI, 2000 400052/34.

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons

Example, Page 1 120pp, English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disorders of the CNS e.g. glioma, glioblastoma, medulloblastoma, neurofibrosarcoma, spindleoma, fibrosarcoma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease. The patent also relates to Nogo activity which can be used to treat or prevent hypoproliferative or benign dysproliferative disorders e.g. fibrosarcoma and tissue hypertrophy. Filigines or antisense Nogo nucleic acids can be used to inhibit proliferation of CNS cells to induce regeneration of neurons. The patent also relates to the plasticity of the CNS in the absence of neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predicting treatment of disorders and to induce neurite growth which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG-D2, NIG-D1 and Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the 144-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 684 AA;

Query Match 100.0% Score 99; DB 21; Length 684;  
Best Local Similarity 100.0%; Pred. No. 5,56 06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 SYDSIKLEPENPPYEBA 350  
AAV71310  
444 SYDSIKLEPENPPYEBA 350

AAV71310 standard, Protein, 684 AA;  
AAV71310

06 NOV 1999 09:05:01

For N. A. protein fragment used in the construction of mutant NIG-D2.

Pat. neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
central nervous system; neoplastic disease; antiproliferative; glioma;  
neurofibrosarcoma; fibrosarcoma; meningioma; neuroblastoma;  
retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
hypoproliferative disorder; benign dysproliferative disorder; disease;  
neurofibrosarcoma; tissue hypertrophy; neuronal regeneration; treatment;  
structural plasticity; screening; mutant; myelin.

OS Rattus sp.

PN WO2000031235-A2.

XX 02-JUN-2000.

XX 05-NOV-1999; 55WD-US26160.

XX 06 NOV 1999; 0905 0107446.

PA (SCHW/) SCHWAB M E.

PI (CHEN/) CHEN M S.

PI Schwab ME, Chen MS;

XX WPI, 2000 400052/34.

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons

Example, Page 1 120pp, English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disorders of the CNS e.g. glioma, glioblastoma, medulloblastoma, neurofibrosarcoma, spindleoma, fibrosarcoma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease. The patent also relates to Nogo activity which can be used to treat or prevent hypoproliferative or benign dysproliferative disorders e.g. fibrosarcoma and tissue hypertrophy. Filigines or antisense Nogo nucleic acids can be used to inhibit proliferation of CNS cells to induce regeneration of neurons. The patent also relates to the plasticity of the CNS in the absence of neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predicting treatment of disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG-D2, NIG-D1 and Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the 144-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

XX Sequence 695 AA;

Query Match 100.0% Score 99; DB 21; Length 695;  
Best Local Similarity 100.0%; Pred. No. 5,66 06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSIKLEPENPPYEBA 18

Db 452 SYDSIKLEPENPPYEBA 469

RESULT 10  
AAV71399  
ID AAV71399 standard, Protein, 732 AA.



AAV71399;  
02-NOV-2000 (first entry)

Rat Nogo A protein fragment used in the construction of mutant NiG-D18.

Rat; neurite growth inhibitor; Nogo A, neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperproliferative disorder; benign dysproliferative disorder; diagnosis; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutein.

Rattus sp.

Key Location/Qualifiers  
Region 1..18  
/note= "Corresponds to residues 172-189 of Nogo A sequence shown in AAV71310"  
Region 19..732  
/note= "Corresponds to residues 261-974 of Nogo A sequence shown in AAV71310"

WO2000031235-A2.

02-JUN-2000

05-NOV 1999; 99WO-US26160

06-NOV-1998; 98US-0107446.

(SCHWAB/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000 400052/34

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page -; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NiG-D18. NiG-D18 is composed of His-tag/TT tag/His-A sequence aa 172-189 + 261-974/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH-3T3 fibroblast spreading.  
Note: The present sequence is not given in the specification but is

CC derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42  
CC are referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However, the specification does not include sequences for  
CC these SEQ ID numbers.

XX Sequence 732 AA;

Query Match 100.0% Score 100, E-21; Length 732;  
Best Local Similarity 100.0%, Fred. No. 5.3e-06;  
Matches 18; Conservative 0, Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSIKLEPNPPPYEEA 18  
|||||  
Db 381 SYDSIKLEPNPPPYEEA 398

RESULT 11

AAV71398  
ID AAV71398 standard; Protein; 736 AA.

XX AAV71398;

AC AAV71398;

DT 02-NOV-2000 (first entry)

XX

DE

XX

KW

KW

KW

KW

KW

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KW

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KW

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KW

KW

Rattus sp.

Key Location/Qualifiers  
Region 1..18  
/note= "Corresponds to residues 172-189 of Nogo A sequence shown in AAV71310"  
Region 19..732  
/note= "Corresponds to residues 257-974 of Nogo A sequence shown in AAV71310"

WO2000031235-A2.

02 JUN 2000.

05-NOV-1999; 99WO-US26160.

06-NOV-1998; 98US-0107446.

(SCHWAB/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000 400052/34.

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page -; 122pp; English.

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's

therapeutic. Therapeutics which promote Nogo activity can be used to treat or prevent hyperplastic or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in direct or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present invention is derived by fusing two fragments of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG-D1. NIG-D1 is composed of:

1. Amino acids 172-183 + 257-374/His tag.

2. Nogo A deletion mutants were used for mapping the inhibitory region of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-374, particularly amino acids 142-222. In addition, N terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Notes: The present sequence is not given in the specification but is believed to be the Nogo A sequence shown in AAV71310. SEQ ID numbers 15-47 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 746 AA.

Query Match: 100.0%, Score 99, DB 21, Length 737, Best Local Similarity 100.0%, Freq. No. 5.9e-06, Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

1 SYDSIKLEPENPPYEEA 18  
10 SYDSIKLEPENPPYEEA 18  
18 SYDSIKLEPENPPYEEA 469

Query Match: 100.0%, Score 99, DB 21, Length 737, Best Local Similarity 100.0%, Freq. No. 5.9e-06, Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

AAV71310: 18 SYDSIKLEPENPPYEEA 18  
AAV71310: 10 SYDSIKLEPENPPYEEA 18  
AAV71310: 18 SYDSIKLEPENPPYEEA 469

AAV71310: 18 SYDSIKLEPENPPYEEA 18

Pat Nogo A protein fragment used in the construction of mutant NIG-D1.

Pat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperplastic; tissue hypertrophy; benign dysproliferative disorders; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutagen.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

Patent sp.

XX Example, Page 1, 122pp, English.

XX The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, neuroblastoma, meningioma, retinoblastoma, neuroblastoma, glioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperplastic or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present invention is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG-D1. NIG-D1 is composed of:

1. Amino acids 172-183 + 257-374/His tag.

2. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo A protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-374, particularly amino acids 142-222. In addition, N terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Notes: The present sequence is not given in the specification but is believed to be the Nogo A sequence shown in AAV71310. SEQ ID numbers 15-47 are referred in claim 32 and SEQ ID NO. 23 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 737 AA:

Query Match: 100.0%, Score 99, DB 21, Length 737, Best Local Similarity 100.0%, Freq. No. 5.9e-06, Matches 18, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 SYDSIKLEPENPPYEEA 18  
Db 452 SYDSIKLEPENPPYEEA 469

RESULT 13

AAV71310: 18 SYDSIKLEPENPPYEEA 18

AAV71310: 10 SYDSIKLEPENPPYEEA 18

AAV71310: 18 SYDSIKLEPENPPYEEA 469

Pat Nogo A protein fragment used in the construction of mutant NIG-D1.

Pat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS; central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; degenerative nerve disease; Alzheimer's disease; Parkinson's disease; hyperplastic; tissue hypertrophy; benign dysproliferative disorders; psoriasis; tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutagen.

Rattus sp.

Location/Qualifiers

Region

Region

Region

Region

/note "Corresponds to residues 172-374 of Nogo A sequence shown in AAV71310"

64-746

/note "Corresponds to residues 222-374 of Nogo A sequence shown in AAV71310"

W02000031235-A2.

02-JUN-2000

05-NOV-1999; 09WO-US026160

06-NOV-1998; 98US-0107446.

(SCHWAB/) SCHWAB M E.  
(CHEN/) CHEN M S.

Schwab ME, Chen MS;

WPI; 2000-400052/34

Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page -; 122pp; English

The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is derived by fusing two fragments of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG-D2. NIG-D2 is composed of His-tag/T7 tag/Nogo A sequence aa 172-234 + 292-974/His-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 25-42 are referred in claim 30 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

Sequence 746 AA;

Query Match 100.0%; Score 99; DB 21; Length 746;  
Best Local Similarity 100.0%; Pred No 6e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SYDSIKLEPENPPYEEA 19  
|||||  
395 SYDSIKLEPENPPYEEA 412

BLT 14

1562  
AAV71562 standard; Protein; 803 AA

AAV71562;

02-NOV-2000 (first entry)

Fat Nogo A protein fragment used in the construction of mutant NIG.

XX Rat; neurite growth inhibitor; Nogo A, neural cell, myelin, CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma, meningioma, retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.

OS Rattus sp.

XX W02000031235 A2.

XX 02-JUN-2000

XX 05-NOV-1999; 09WO-US026160.

XX 06-NOV-1998; 98US-0107446.

XX (SCHWAB/) SCHWAB M E.  
XX (CHEN/) CHEN M S.

XX Schwab ME, Chen MS;

XX WPI; 2000 400052/34.

XX Nogo proteins and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons -

Example; Page -; 122pp; English.

CC The patent relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nig nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of rat Nogo A protein shown in AAV71310, which is used in the construction of mutant NIG. The mutant is composed of His-tag/T7-tag/Nogo A sequence aa 172-974/His-tag.

CC Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 542-722. In addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3 fibroblast spreading.

CC Note: The present sequence is not given in the specification but is derived from rat Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 30 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

SQ Sequence 803 AA;

Query Match 100.0%; Score 99; DB 21; Length 803;  
Best Local Similarity 100.0%; Pred No 6e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SYDSIKLEPENPPYEEA 18  
|||||  
DB 452 SYDSIKLEPENPPYEEA 469

AAV71310 structure; protein; 974 AA.  
AAV71310;

12 NOV 2003 (first entry)

But Nogo A protein fragment used in the construction of mutant N1next.

But, neurite growth inhibitor, Nogo A, neural cell, myelin, CNS, central nervous system; neoplastic disease; antiproliferative; glioma; antisense gene therapy; neuroblastoma; meningioma; retinoblastoma; developmental nerve disease; Alzheimer's disease; Parkinson's disease; hypoproliferative disease; benign dysproliferative disorder; diagnosis; transplant tissue hypertrophy; neuronal regeneration; treatment; structural plasticity; screening; mutant; mutant; mutant.

protein sp.

W 09 41:45 AA

12 NOV 2003

12 NOV 2003 00W US261601

12 NOV 2003 00W 0107446

12 NOV 2003 00W 0107446

12 NOV 2003 00W 0107446

12 NOV 2003 00W 0107446

12 NOV 2003 00W 0107446

Nogo protein and nucleic acids useful for treating neoplastic disorders of the central nervous system and inducing regeneration of neurons.

Example: Page 124pp English.

The present relates to neurite growth inhibitor Nogo which is free of all central nervous system (CNS) myelin material with which it is naturally associated. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disorders of the CNS such as glioma, glioblastoma, medulloblastoma, astrocytoma, oligodendroglioma, meningioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's disease. Therapies which promote Nogo activity can be used to treat or prevent hypoproliferative or benign dysproliferative disorders e.g. fibrosis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. The present sequence is a fragment of the Nogo A protein shown in AAV71310, which is used in the construction of mutant N1next. The mutant is composed of his 141/173 (aa/aa) Nogo A sequence aa 1-374/173-tag. Nogo A deletion mutants were used for mapping the inhibitory sites of Nogo protein. Major inhibitory region was identified in the Nogo A sequence from amino acids 172-974, particularly amino acids 142/172. In addition, N terminal region 1-171 was found to be inhibitory to N1H-93 fibroblast spreading.

Notes: The present sequence is not given in the specification but is derived from the Nogo A sequence shown in AAV71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID No. 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers.

SO Sequence 974 AA;

Query Match

Best Local Similarity 100.0%; Score 99; DB 21; Length 974;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSIKLEPENPPPYEEA 18

DB 623 SYDSIKLEFENPPPYEEA 640

Search completed: January 24, 2003, 11:10:33  
Job time: 36 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

protein - protein search, using sw model

January 24, 2003, 11:09:39 : Search time 15 seconds  
(without alignments)  
115.361 Million cell updates/sec

US-09-893-348-19

Effect score: 99  
Sequence: 1 SYDSIKLEPENPPPYEEA 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_73:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	51	51.5	2957	2	T33152	hypothetical prote
2	50	50.5	442	2	S58738	nitrate-binding pr
3	50	50.5	473	2	A56377	rubber particle cy
4	49	49.5	458	2	AF2165	bicarbonate transp
5	49	49.5	1398	2	T25568	hypothetical prote
6	48.5	49.0	307	2	T40240	dimethylase - firs
7	48.5	49.0	315	2	T43249	rRNA (adenine-N6,N
8	48	48.5	90	1	ZNXPLC	zinc finger protei
9	47	47.5	257	2	F75084	hypothetical prote
10	47	47.5	591	2	T41531	activator of Hsp70
11	47	47.5	591	2	T51996	hypothetical prote
12	46	46.5	141	2	PC4230	peroxisome prolif
13	46	46.5	156	2	T18755	hypothetical prote
14	46	46.5	156	2	FR9418	protein B9413.7 (i
15	46	46.5	330	2	G83853	spore cortex lytic
16	46	46.5	340	2	T49887	hypothetical prote
17	46	46.5	475	2	JC4264	peroxisome prolif
18	46	46.5	505	2	A54101	peroxisome prolif
19	46	46.5	505	2	JC4859	peroxisome prolif
20	46	46.5	539	2	T21816	hypothetical prote
21	46	46.5	1113	2	T20140	hypothetical prote
22	45	45.5	317	2	T00986	yeast pheromone re
23	45	45.5	400	2	T29121	hypothetical prote
24	45	45.5	459	2	G83784	glycerol-3-phospha
25	45	45.5	465	2	A44498	radial spoke prote
26	45	45.5	475	2	JE0279	peroxisome prolif
27	45	45.5	477	2	C42214	peroxisome prolif
28	45	45.5	487	2	JC2495	histamine H1 recep
29	45	45.5	504	2	JE0280	peroxisome prolif

30	45	45.5	505	2	JC5777	peroxisome prolif
31	44.5	44.9	211	2	C82748	stringent starvati
32	44	44.4	194	2	T22209	hypothetical prote
33	44	44.4	250	2	S36769	ubiquitin-protein
34	44	44.4	413	2	T02463	hypothetical prote
35	44	44.4	423	2	A30819	interferon regulat
36	44	44.4	446	2	S77389	nitrate transport
37	44	44.4	483	2	T24856	hypothetical prote
38	44	44.4	520	2	G88846	protein T12A7.2 (i
39	44	44.4	613	2	T00853	hypothetical prote
40	44	44.4	631	2	A31203	interferon-regulat
41	44	44.4	661	2	T15073	hypothetical prote
42	44	44.4	754	2	A56619	female sterile hom
43	44	44.4	2434	2	S44861	DNA topoisomerase
44	44	44.4	3951	1	VFIHB1	F1 protein - avian
45	43.5	43.9	174	2	F75097	adenyllylsulfate 3-

#### ALIGNMENTS

##### RESULT 1

T33152

hypothetical protein T04D1.4 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29 Oct 1999

C/Accession: T33152

R/Davidson, S.; Wohldmann, P.

submitted to the EMBL Data Library, May 1998

A/Description: The sequence of C. elegans cosmid T04D1.

A/Reference number: 221292

A/Accession: T33152

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2957 <DAV>

A/Cross-references: EMBL:AF067617; PIRN:AAQ17569 1; GSPFR:GN000019; CESP:T04D1.4

A/Experimental source: strain Bristol N2; clone T04D1

C/Genetics:

A/Gene: CESP:T04D1.4

A/Map position: 1

A/Introns: 122/3; 293/3; 515/3; 1205/2; 1577/1; 2221/3; 2776/1; 2864/3

##### Query Match

Best Local Similarity 51.5%; Score 51; DB 2; Length 2957;

Matches 7; Conservativity 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 IKLEPENPPPYEE 17

Db 464 VKMEPEKSPYQ 476

##### RESULT 2

S58738

nitrate-binding protein nrtA precursor, periplasmic [similarity] - Phormidium lamosum

C/Species: Phormidium lamosum

C/Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Oct-2000

C/Accession: S58738; S56641; S62124

R/Merchan, F.; Kindle, K.L.; Llana, M.J.; Serra, J.L.; Fernandez, E.

Plant Mol. Biol. 28, 759-766, 1995

A/Title: Cloning and sequencing of the nitrate transport system from the thermophilic, f

cus sp. PCC 7942.

A/Reference number: S58738; MUID:95375238; PMID:7647306

A/Accession: S58738

A/Molecule type: DNA

A/Residues: 1-442 <MER>

A/Cross-references: EMBL:U19598; NID:G114890; PIRN:GA079656 1; PIR:G119393; R/Merchan, F.; Prieto, R.; Kindle, K.L.; Llana, M.J.; Serra, J.L.; Fernandez, E.

Plant Mol. Biol. 27, 1037-1042, 1995

A/Title: Isolation, sequence and expression in Escherichia coli of the nitrate reductase

A/Reference number: S56640; MUID:95284340; PMID:7766873

A/Accession: S56641

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA





Residues: 1-315 <HOU>  
 Cross-references: EMBL:Z68293, PIDN:CAA92585.1  
 Genetics:  
 Note: DIM1  
 Function:  
 Description: dimethylation of two adjacent adenosines from the 3' end of the 16S rRNA  
 Superfamily: rRNA (adenine-N6-)-methyltransferase  
 Keywords: methyltransferase

Query Match 49.0%, Score 45.5; DB 2; Length 315;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 Matches 8; Conservative 5; Mismatches 0; Indels 3; Gaps 1;  
 5 IKLEPENPF--YEE 17  
 ::|||:|||:|  
 201 VRIEPKNPPPLAFEE 216

ULT 8  
 PLC  
 c finger protein - lymphocytic choriomeningitis virus (strain Armstrong 53b)  
 Species: lymphocytic choriomeningitis virus  
 Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
 Accession: A32592  
 alvato, M.S.; Shimomaye, E.M.  
 ology 173, 1-10, 1989  
 Title: The completed sequence of lymphocytic choriomeningitis virus reveals a unique R  
 Reference number: A32592, NCID:30051057, PMID:2510401  
 Accession: A32592  
 Molecule type: genomic RNA  
 Residues: 1-90 <SAL>  
 Cross-references: GB:M7673, NID:G331385, PIDN:AAA46268.1, PID:G331386  
 Comment: This protein may act as an RNA-binding protein.  
 Genetics:  
 Map position: segment L  
 Superfamily: arenavirus zinc finger protein  
 Keywords: RNA binding; zinc finger  
 2-54/Region. zinc finger CCCC motif

Query Match 48.5%, Score 48; DB 1; Length 90;  
 Best Local Similarity 61.5%; Pred. No. 3.7;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 5 IKLEPENPPYEE 17  
 | | | | | | | |  
 78 ISTAPSSPPPYEE 90

ULT 9  
 084  
 othetical protein PAB1661 - Pyrococcus abyssi (strain Orsay)  
 Species: Pyrococcus abyssi  
 Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
 Accession: F75084  
 onymus, Genoscope  
 mitted to the EMBL Data Library, July 1999  
 Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
 Reference number: A75001  
 Accession: F75084  
 Status: preliminary  
 Molecule type: DNA  
 Residues: 1-257 <KAW>  
 Cross-references: GB:AJ248286; GB:AL096836; NID:G5458366; PIDN:CAB49979.1; PID:G545849  
 Experimental source: strain Orsay  
 Genetics:  
 Superfamily: Pyrococcus abyssi hypothetical protein PAB1661

Query Match 47.5%, Score 47; DB 2; Length 257;  
 Best Local Similarity 61.5%; Pred. No. 17;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 2 YDSIKLEPENPF 14

Db 227 FMSYKLEPKNPVP 239

RESULT 10  
 T41531  
 activator of Hsp70 and Hsp90 chaperones - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
 C/Accession: T41531  
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.  
 submitted to the EMBL Data Library, March 1999  
 A/Reference number: Z22000  
 A/Accession: T41531  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-591 <WOO>  
 A/Cross-references: EMBL:AL049498; PIDN:CAB39910.1; GSPDR:GN00068; SPDB:SPCC645.14c  
 A/Experimental source: strain 972h-; cosmid c645  
 C/Genetics:  
 A/Gene: SPDB:SPCC645.14c  
 A/Map position: 3  
 C/Superfamily: unassigned tetratricopeptide repeat proteins; tetratricopeptide repeat hom

Query Match 47.5%, Score 47; DB 2; Length 591;  
 Best Local Similarity 55.6%; Pred. No. 43;  
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SYDSIKLEPENPPYEEA 18  
 | | | | | | | | | |  
 Db 222 SADSAPKPTTNPFPQQA 239

RESULT 11  
 T51996  
 hypothetical protein stil+ - fission yeast (Schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
 C/Accession: T51996  
 R:Yamashita, Y.; Nakaseko, Y.; Samejima, T.; Kurada, K.; Yamada, H.; Yanagida, M.  
 Nature 384, 276-279, 1996  
 A/Title: 20S cyclosome complex formation and proteolytic activity inhibited by the cAMP/1  
 A/Reference number: Z25896  
 A/Accession: T51996  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-591 <YAM>  
 A/Cross-references: EMBL:DB5197; PIDN:BAA22619.1  
 C/Genetics:  
 A/Gene: stil+

Query Match 47.5%, Score 47; DB 2; Length 591;  
 Best Local Similarity 55.6%; Pred. No. 43;  
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SYDSIKLEPENPPYEEA 18  
 | | | | | | | | | |  
 Db 222 SADSAPKPTTNPFPQQA 239

RESULT 12  
 PC4290  
 peroxisome proliferator activated receptor gamma 2 - human (fragment)  
 N/Alternate names: peroxisome proliferator activated receptor gamma 1  
 C/Species: Homo sapiens (man)  
 C/Date: 07-Jul-1997 #sequence\_revision 18-Jul-1997 #text\_change 17-Mar-1999  
 C/Accession: PC4290  
 R:Yanase, T.; Yashiro, T.; Takitani, K.; Kato, S.; Taniguchi, S.; Takayanagi, R.; Nawata, M.  
 Biochem Biophys Res Commun 233, 320-324, 1997  
 A/Title: Differential expression of PPAR gamma 1 and gamma 2 isoforms in human adipose ti  
 A/Reference number: PC4290; MUID:97289627, PMID:9144532  
 A/Accession: PC4290  
 A/Molecule type: mRNA



GenCore version 5.1.3  
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Protein - protein search, using sw model

Query: US-09-893-348-19  
Search time 10 seconds  
(without alignments)  
74.657 Million cell updates/sec

Effect score: 99

Sequence: 1 SYDSIKLEPPNPPEEA 18

oring table: BLOSUM62

Gapop 10.0, Gapext 0.5

arched: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

imum DB seq length: 0  
imum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ID	Score	Query Match	Length	DB ID	Description
1	99	100.0	1163	1 PTM4 PAT	Q9JH11 ratius norv
2	95	97.9	1192	1 PTM4_HUMAN	Q9NGG3 homo sapien
3	48	48.5	90	1 ZNFP_LYCVIA	P18541 lymphocytic
4	47	47.5	591	1 ST11_SCHPO	Q9US15 schizosacch
5	46	46.5	413	1 HXN3_CHICK	Q93353 gallus gall
6	46	46.5	443	1 HXN3_HUMAN	Q43365 homo sapien
7	46	46.5	443	1 HXN3_MOUSE	P02831 mus musculu
8	46	46.5	475	1 PPAT_CRIGR	P57797 cricetus
9	46	46.5	475	1 PPAT_PARIT	Q19052 cyrtolagus
10	46	46.5	505	1 PPAT_HUMAN	P37231 homo sapien
11	46	46.5	505	1 PPAT_MACMU	Q18924 macaca mula
12	46	46.5	505	1 PPAT_MOUSE	P37234 mus musculu
13	46	46.5	505	1 PPAT_RAT	O88275 rattus norv
14	45	45.5	465	1 RSP4_CHLRF	Q01656 chlamydomon
15	45	45.5	477	1 PPAT_XENLA	P37234 xenopus lae
16	45	45.5	487	1 HHIP_HUMAN	P35367 homo sapien
17	45	45.5	504	1 PPAT_PIG	O62807 sus scrofa
18	45	45.5	505	1 PPAT_BOVIN	Q19971 bos taurus
19	44	44.4	250	1 YBGE_YEAST	F33796 saccharomyc
20	44	44.4	446	1 NPTA_SYNY3	F73452 synethecyst
21	44	44.4	631	1 MX1_MOUSE	P09922 mus musculu
22	44	44.4	800	1 T2D4_HUMAN	Q15542 homo sapien
23	44	44.4	801	1 BPB2_HUMAN	P25440 homo sapien
24	44	44.4	1114	1 TP2M_CABEU	P34534 caenorhabdi
25	44	44.4	1951	1 VSP1_PBYB	P37920 avian infec
26	43.5	43.9	174	1 CYSC_PYPAB	P56858 pyrococcus
27	43	43.4	265	1 PSAT_TRYCR	P92188 trypanosoma
28	43	43.4	304	1 YQNI_CABEU	Q09522 caenorhabdi
29	43	43.4	334	1 FLS_EUSGR	Q9m547 eustoma gra
30	43	43.4	337	1 FLS_MALDO	Q9xhg2 malus domes
31	43	43.4	348	1 FLS_PETHY	Q07512 petunia hyb
32	43	43.4	349	1 FLS_SOLTU	Q41452 solanum tub
33	43	43.4	440	1 NRTA_ANASP	Q44292 anabaena sp

34	43	43.4	443	1 NRTA_SYNY3	F33796 saccharomyc
35	43	43.4	546	1 Y341_HUMAN	Q15049 homo sapien
36	43	43.4	601	1 Y656_CHLIR	Q94966 chlamydia t
37	43	43.4	789	1 PL5B_MYCTU	O53207 mycobacteri
38	43	43.4	1787	1 CHD3_CABEU	Q22516 caenorhabdi
39	42	42.4	65	1 VF08_VACCV	P34360 vaccinia vi
40	42	42.4	372	1 HMEN_POMMC	P07703 pomoxys mori
41	42	42.4	464	1 TFEI_METTH	Q07703 pomoxys mori
42	42	42.4	489	1 YN98_YEAST	P53705 saccharomyc
43	42	42.4	678	1 PTP2_YEAST	P43606 saccharomyc
44	42	42.4	703	1 ML51_HUMAN	Q15234 homo sapien
45	42	42.4	910	1 PPP1_PAT	Q61474 rattus norv

## ALIGNMENTS

RESULT 1  
PTM4 PAT STANDARD; PRT; 1163 AA.  
ID RTN4 RAT  
AC Q9JH11; Q9JH10, Q9PD09; Q9WTE9; Q9WTF0;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Fucose)  
DE (Glut4 vesicle 20 kDa protein).  
GN RTN4 OR NOGO.  
OS Rattus norvegicus (Rat).  
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
PN [1]  
PT SEQUENCE FROM N.A. (ISOPFORM 3), AND PARTIAL SEQUENCE.  
RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte.  
RX MEDLINE=99249816; PubMed=10231557;  
RA Morris N.T., Rose S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
PT "Cloning and characterization of a 22 kDa protein from rat adipocytes;  
RT a new member of the reticulon family.";  
PL Biochim. Biophys. Acta 1450:68-76(1999)  
RN [2]  
PP SEQUENCE FROM N.A. (ISOPFORM 1; 2 AND 3)  
RX MEDLINE=20122258; PubMed=10667796;  
RA Chen M.S., Huber A.B., Van der Haar M.R., Frank M., Schnell U.;  
PT Spillmann A.A., Christ P., Schwab M.E.;  
RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
PL antigen for monoclonal antibody IN-1.";  
RN Nature 403:434-439(2000).  
RN [3]  
PP SEQUENCE FROM N.A. (ISOPFORM 2 AND 4).  
PP STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
RA Ito T., Schwartz S.M.;  
PT "Cloning of a member of the reticulon gene family in rat: one of two  
RT minor splice variants.";  
PL Submitted (FPI-1999) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (by  
CC similarity).  
CC -!- SUBUNIT: Interacts with Bcl-x1 and Bcl 2 (by similarity).  
CC -!- SUPPLEMENTARY INFORMATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -!- ALTERNATIVE PRODUCTS: 4 isoforms, isoform 1/Megs A/Nr 220 250  
CC (shown here), 2/Megs-B/Fucose-M1, 3/Megs C/VF02 and 4/Fucose M2;  
CC are produced by alternative splicing.  
CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in brain  
CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are  
CC present in dorsal root ganglion, sciatic nerve and P012 cells  
CC after longer exposure. Isoforms 2 and 3 are detected in kidney,  
CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high  
CC level in skeletal muscle. In adult animals isoform 1 is expressed  
CC mainly in the nervous system.  
CC -!- SIMILARITY: CONTAINS 1 RETICULON DOMAIN.  
CC





TISSUE=Testis;  
Sha J.H., Zhou Z.M., Li J.M.;  
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
[14]  
TOPOLOGY.  
TISSUE=Brain;  
MEDLINE:20129259; PubMed:10667797;  
Grandpre T., Nakamura F., Vartanian T., Stillmatter S.M.;  
"Identification of the Nogo inhibitor of axon regeneration as a  
reticulation protein";  
Nature 403:439-444(2000).  
-1- FUNCTION. Potent neurite outgrowth inhibitor which may also help  
block the regeneration of the nervous central system in adults.  
Isoform 2 reduces the anti-apoptotic activity of Bcl-x1 and Bcl-2.  
This is likely consecutive to their change in subcellular  
location, from the mitochondria to the endoplasmic reticulum,  
after binding and sequestration.  
-1- SUBUNIT. Interacts with Bcl-x1 and Bcl-2.  
-1- SUBCELLULAR LOCATION. Integral membrane protein. Endoplasmic  
reticulum. Anchored to the membrane of the endoplasmic reticulum  
through 2 putative transmembrane domains.  
-1- ALTERNATIVE PROCTYTS: 4 isoforms, 1/RTN 4A/Nogo-A/RIN-XL (shown  
here), 2/RTN 4B/Nogo-B/RTN-XS/Foocen-M, 3/RTN 4C/Nogo-C/Foocen-  
S and 4; are produced by alternative splicing.  
-1- TISSUE SPECIFICITY. Isoform 1 is specifically expressed in brain  
and testis and weakly in heart and skeletal muscle. Isoform 2 is  
widely expressed excepted for the liver. Isoform 3 is expressed in  
brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
specific.  
-1- SIMILARITY: CONTAINS 1 RETICULON DOMAIN.  
-1- CAUTION: Ref.11 sequence differs from that shown due to  
frameshifts in positions 1149 and 1156.  
-----  
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-----  
EMBL; AJ251383; CAB99248.1; -  
EMBL; AJ251384; CAB99249.1; -  
EMBL; AJ251385; CAB99250.1; -  
EMBL; AB040462; BAB19227.1; -  
EMBL; AB040463; BAB18928.1; -  
EMBL; AF148537; AAG12176.1; -  
EMBL; AF148538; AAG12177.1; -  
EMBL; AF087901; AAG12205.1; -  
EMBL; AF320999; AAG40878.1; -  
EMBL; AF132047; AAD31021.1; -  
EMBL; AF132048; AAD31022.1; -  
EMBL; AB015639; BAA83712.1; -  
EMBL; AF077050; AAD27783.1; -  
EMBL; AF177332; AAG17076.1; -  
EMBL; AB020693; BAA74909.1; -  
EMBL; BC001035; AAH01035.1; -  
EMBL; BC007109; AAH07109.1; -  
EMBL; BC014366; AAH14366.1; -  
EMBL; BC012619; AAH12619.1; -  
EMBL; BC010737; AAH10737.1; -  
EMBL; AF125103; AAD39920.1; ALT FRAME.  
EMBL; AF063601; AAG33160.1; ALT\_FRAME.  
EMBL; AF333336; AAK20831.1; ALT\_FRAME.  
Genew; HGMG:14085; RTN4.  
MIM; 604475;  
InterPro; IPR003388; Reticulon.  
pfam; PF02453; Reticulon, 6.  
PROSITE; PS50845; RETICULON; 1.  
Endoplasmic reticulum; Alternative splicing; Transmembrane.  
DOMAIN 1 1018 CYTOPLASMIC (POTENTIAL).  
TRANSMEM 1019 1039 POTENTIAL.  
DOMAIN 1040 1133 LUMENAL (POTENTIAL).

FT TRANSMEM 1134 1154 POTENTIAL.  
FT DOMAIN 1155 1192 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 1005 1192 RETICULON.  
FT DOMAIN 30 47 POLY-GLU.  
FT DOMAIN 143 148 POLY-PRO.  
FT VARSPPLIC 1 993 MISSING (IN ISOFORM 3).  
FT VARSPPLIC 994 1004 AIFSALISKTS -> MDGQFFWTFP (IN ISOFORM  
3).  
FT VARSPPLIC 58 289 MISSING (IN ISOFORM 4).  
FT VARSPPLIC 186 1004 MISSING (IN ISOFORM 2).  
FT CONFLICT 107 107 S -> C (IN REF. 6).  
FT CONFLICT 135 135 E -> Q (IN REF. 6).  
FT CONFLICT 458 458 S -> P (IN REF. 1).  
FT CONFLICT 564 564 N -> S (IN REF. 13).  
FT CONFLICT 684 699 NAALQETAPYISIAQ -> MQLEPKQYLILYLIHV  
(IN REF. 5).  
SQ SEQUENCE 1192 AA; 129930 MW; CDE234RBF15RAC7A CF064;  
Query Match Score 85; DB 1; Length 1192;  
Best Local Similarity 83.3%; Pred. No. 7.6e-05;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SYDSIKLEPENPPYEEA 18  
Db 645 NYESIKHEPENPPYEEA 662  
-----  
RESULT 3  
ZNF\_LYCVA  
ID ZNF\_LYCVA STANDARD; PRT; 90 AA.  
AC P18541;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Zinc finger protein.  
GN Z.  
OS Lymphocytic choriomeningitis virus (strain Armstrong).  
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.  
OX NCBI\_TaxID=11624;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90051057; PubMed.2510401,  
RA Salvato M.S., Shumway E.M.;  
RT "The completed sequence of lymphocytic choriomeningitis virus reveals  
a unique RNA structure and a gene for a zinc finger protein.";  
RL Virology 173:1-10(1989).  
CC -1- FUNCTION: MIGHT BE AN RNA-BINDING PROTEIN WITH A REGULATORY ROLE.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; M27693; AAA46268.1; -  
CC PIR; A32592; ZNXPIC.  
CC InterPro; IPR000822; Znf\_C2H2.  
CC ProDom; PD020016; Znf\_P11.  
CC PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
KW zinc-finger; RNA-binding.  
FT ZN\_FING 32 53  
SQ SEQUENCE 90 AA; 10184 MW; D2EAF9EC2287E4EA CRC64;  
Query Match Score 49; DB 1; Length 90;  
Best Local Similarity 61.5%; Pred. No. 1.4;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 5 IKLEPENPPYEE 17  
Db 78 ISTAPSSPPYEE 90

1. SCHPO STANDARD; PRT; 591 AA.  
16-OCT-2001 (Rel. 40, Created)  
16-OCT-2001 (Rel. 40, Last sequence update)  
15-JUN-2002 (Rel. 41, Last annotation update)  
Heat shock protein 70 homolog.  
STILL OR STILL OR SHOCK645.140.  
Schizosaccharomyces pombe (Fission yeast).  
Fukuyama T, Pineda A, Yaguchi A, Schizosaccharomycetes,  
Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
Schizosaccharomycetes  
NCBI TaxID=4896;  
[1]  
SEQUENCE FROM N.A.  
Yamashita T, Nakano Y, Gotoh T, Furuta F, Yamada H,  
Yamashita M;  
Submitted (MAY 1996) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
STRAIN=972;  
MEDLINE=0184401; PubMed=1859160;  
Wood V, Gwilliam R, Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
Stourac V., Pear N., Hayles C., Baker S., Basham D., Bowman S.,  
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
Gentles A., Gilbert A., Hamilton N., Harris D., Hedges G., Hodgson G.,  
Holroyd S., Hornsby T., Howarth S., Huckle R., Hunt S., Jags K.,  
James K., Jones K., Jones M., Leather S., McDonald S., McLean G.,  
Mooney P., Mouton R., Murali K., Murphy L., Nibbel T., Odell C.,  
Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
Skellton G., Symonds M., Squares P., Squares S., Stevens K.,  
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
Woodward J., Young L., Young T., Ait F., Rutter J., Gilmour R.,  
Wolfe J., Vansteele E., Rieger M., Schaefer M., Mueller-Auer S.,  
Gabel C., Fuchs M., Fritz G., Holzer F., Moestl D., Hilbert H.,  
Borzym K., Burger I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
Telford A., Gellera E., Duan S., Givov S., Delaunay V., Mottier S.,  
Dallport F., Aves S., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
Jocan M., Rader M., Gallard C., Tullia V.A., Garzon A., Thode G.,  
Datta P.R., Cruzado L., Jimenez J., Sanchez M., del Pey F., Benito G.,  
Domiguez A., Revuelta J., Moreno S., Armstrong J., Forsburg S.L.,  
Darrat L., Low T., McCombie W.R., Paulsen O., Potashkin J.,  
Shpakowski G.V., Hestery P., Barrett R.G., Nurse P.;  
"The genome sequence of Schizosaccharomyces pombe";  
Nature 415:871-880(2002).  
[3]  
FUNCTION: MAY PLAY A ROLE IN MEDIATING THE HEAT SHOCK RESPONSE  
OF SOME HSP70 GENES (BY SIMILARITY).  
SUBUNIT: PART OF A LARGER COMPLEX THAT INCLUDES HSP70, HSP90, AND  
IMMUNOPHILINS (BY SIMILARITY).  
[4]  
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
[5]  
SIMILARITY: CONTAINS 9 TPR REPEATS.  
  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
  
EMBL: D85197; BAA22619.1;  
EMBL: AL049496; CAB39910.1;  
HSP70; P03417; IAI7;  
InterPro: IPR01440; TPR;  
Pfam: PF00615; TPR; 8;  
SMART: SM00028; TPR; 7;  
Heat shock; TPR repeat; Repeat.

EMBL: D85197; BAA22619.1;  
EMBL: AL049496; CAB39910.1;  
HSP70; P03417; IAI7;  
InterPro: IPR01440; TPR;  
Pfam: PF00615; TPR; 8;  
SMART: SM00028; TPR; 7;  
Heat shock; TPR repeat; Repeat.

FT REPEAT 2 35 TPR 1.  
FT REPEAT 37 69 TPR 2.  
FT REPEAT 70 103 TPR 3.  
FT REPEAT 265 298 TPR 4.  
FT REPEAT 299 331 TPR 5.  
FT REPEAT 339 372 TPR 6.  
FT REPEAT 399 432 TPR 7.  
FT REPEAT 434 466 TPR 8.  
FT REPEAT 467 500 TPR 9.  
FT CONFLICT 28 28 A > T (IN REF. 1).  
SQ SEQUENCE 591 AA, 4544 MW, 52140.70=44484AA CRC64,  
  
Query Match 47.5% Score 47, E3 1, Length 591;  
Best Local Similarity 55.0% (Fied. No. 15;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
  
OY 1 SYDSIKLEPENPPYEBA 18  
Db 222 SADSAPERTTTPFQFQA 222  
  
RESULT 5  
HXD3 CHICK  
ID HXD3\_CHICK STANDARD; PRT; 413 AA.  
AC 093353;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Homeobox protein Hox-D3.  
GN HXD3 OR HOXD-3.  
OS Gallus gallus (Chicken)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;  
OC Gallus.  
OC NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=3840133; PubMed=2733103;  
PA Sealey P.D., Yutzey K.E.;  
PT "Analysis of Hox gene expression during early avian heart  
development";  
PL Dev. Dyn. 213:82-91(1998).  
CC [1]  
CC FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF  
CC A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH  
CC SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.  
CC [2]  
CC SUBCELLULAR LOCATION: Nuclear.  
CC [3]  
CC SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.  
  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
  
EMBL: AF067959; AAC19377.1;  
DR HSSP; P02833; ISAN.  
DR InterPro; IPR001827; Antennapedia.  
DR InterPro; IPR000047; HTH\_repressor.  
DR InterPro; IPR001356; Homeobox  
Pfam; PF00046; homeobox; 1  
DR PRINTS; PR00025; ANTENNAPEDIA.  
DR PRINTS; PR00024; HOMEBOX  
DR PRINTS; PR00031; HTHREPRESSR.  
DR ProDom; PD000010; Homeobox; 1.  
DR SMART; SM00389; HOX; 1.  
DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS00071; HOMEBOX\_2; 1.  
DR PROSITE; PS00032; ANTENNAPEDIA; 1.  
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;  
KW Transcription regulation.  
FT DNA\_BIND 173 232 HOMEBOX.













--- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
NRI SUBFAMILY.

-----  
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EMBL: AF033103; AAB87480.1; -  
EMBL: AF033343; AAB87482.1; -  
EMBL: AF033342; AAB87481.1; -  
HSSP: P37231; 1FM9.

InterPro: IPR000536; Hormone\_rec\_lig.  
InterPro: IPR001723; Steroid\_receptor.  
InterPro: IPR001628; Znf\_C4steroid.  
Pfam: PF00104; hormone\_rec; 1.  
Pfam: PF00105; zf-C4; 1.  
PRINTS: PR00399; STRDHORMONER.

PRINTS: PR00047; STROIDFINGER.  
ProDom: PD000035; Znf\_C4steroid; 1.  
SMART: SM00430; HOLI; 1.  
SMART: SM00399; ZNF\_C4; 1.

PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.  
Receptor; Transcription regulation; Activator; DNA-binding;  
Nuclear protein, zinc finger; Multigene family; Alternative splicing;  
Phosphorylation.

DNA BIND 139 203 NUCLEAR RECEPTOR-TYPE.

ZN\_FING 139 159 C4-TYPE.

ZN\_FING 176 156 C4-TYPE.

DOMAIN 318 505 LIGAND BINDING (POTENTIAL).

MOD\_RES 112 112 PHOSPHORYLATION (BY MAPK) (BY  
SIMILARITY).

VARSPLIC 1 30 MISSING (IN ISOFORM 1).

SEQUENCE 505 AA, 57599 MW, 41836A621A6F6342 CRC64;

Query Match 46.5%; Score 46; DB 1; Length 505;  
Best local similarity 57.1%; Idet. No. 18;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPENPPYEE 17

105 AIKVEFASPPYSE 118

UNT 12

T\_MOUSE

PPAT\_MOUSE STANDARD; PRT; 505 AA.

P37238; 01-OCT-1994 (rel. 30, created)

16-OCT-2001 (rel. 40, last sequence update)

16-OCT-2001 (rel. 40, last annotation update)

Peroxisome proliferator activated receptor gamma (PPAR-gamma).

PPARG OR NR1C3.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

[1] SEQUENCE FROM N.A. (ISOFORM 2).

TISSUE=Adipose tissue;

MEDLINE=95011536; PubMed=7926726;

Tontoz P., Hu E., Graves R.A., Budavari A.I., Spiegelman B.M.;

"PPAR gamma 2: tissue-specific regulator of an adipocyte enhancer.";

Genes Dev. 8:1224-1234(1994).

[2] SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=BA1B/S; TISSUE=Heart;

MEDLINE=94059089; PubMed=8240342;

Chen F., Law S.W., O'Malley B.W.;

RT existence of five subfamily members.";

RL Biochem. Biophys. Res. Commun. 196:671-677(1993).

RN [3] SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;

RX MEDLINE=94086482; PubMed=8262913;

RA Zhu Y., Alvares K., Huang Q., Rao M.S., Reddy J.K.;

RT "Cloning of a new member of the peroxisome proliferator-activated

RL receptor gene family from mouse liver.";

RN J. Biol. Chem. 268:26817-26820(1993).

[4] SEQUENCE FROM N.A. (ISOFORM 1).

RP TISSUE=Liver;

RX MEDLINE=94316694; PubMed=8041794;

RA Kiewer S.A., Forman B.M., Plumberg B., Ong F.S., Pergmeyer U.,

RA Mangelsdorf D.J., Umesono K., Evans R.M.;

RT "Differential expression and activation of a family of murine

RL peroxisome proliferator-activated receptors.";

RN Proc. Natl. Acad. Sci. U.S.A. 91:7355-7359(1994).

[5] SEQUENCE FROM N.A.

PX MEDLINE=96249427; PubMed=8647948;

RA Vidal-Puig A., Jimenez-Linan M., Lowell B.B., Hamann A., Hu E.,

RA Spiegelman B., Flier J.S., Moller D.E.;

RT "Regulation of PPAR gamma gene expression by nutrition and obesity in

RL rodents.";

RN J. Clin. Invest. 97:2553-2561(1996).

CC -1- FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS

CC HYPOLIPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,

CC THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYLD-OA

CC OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE

CC PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR

CC OF ADIPOCYTE DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.

CC -1- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.

CC -1- STRCELLULAR LOCATION: Nuclear.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, 1 AND 2 (SHOWN HERE); ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADIPOSE TISSUE. ALSO

CC FOUND IN LIVER, SKELETAL MUSCLE, HEART, ADRENAL GLAND, SPLEEN,

CC KIDNEY AND INTESTINE.

CC -1- DEVELOPMENTAL STAGE: IT APPEARS FIRST AT DAY 13 & POSTCONCEPTION,

CC AND INCREASES UNTIL BIRTH.

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.

CC NRI SUBFAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: U09138; AAA62277.1; -

CC EMBL: U01664; AAA62110.1; -

CC EMBL: U01841; AAC52134.1; -

CC EMBL: U10374; AAA19971.1; -

CC PIR: JN0881; JN0881.

CC HSSP: P37231; 1FM9.

CC TRANSFAC: T02529; -

CC MGD: MGI:97747; Pparg.

CC InterPro: IPR000536; Hormone\_rec\_lig.

CC InterPro: IPR001723; Steroid\_receptor.

CC InterPro: IPR001628; Znf\_C4steroid.

CC Pfam: PF00104; hormone\_rec; 1.

CC Pfam: PF00105; zf-C4; 1.

CC PRINTS: PR00398; STRDHORMONER.

CC PRINTS: PR00047; STROIDFINGER.

CC ProDom: PD000035; Znf\_C4steroid; 1.

CC SMART: SM00430; HOLI; 1.

CC SMART: SM00399; ZNF\_C4; 1.

CC PROSITE: PS00031; NUCLEAR\_RECEPTOR; 1.

CC Receptor; Transcription regulation; Activator; DNA-binding;



```

SIMILARITY)
VARSPPLIC 1 30 MISSING (IN ISOFORM 1).
MUTAGEN 112 112 S->A INCREASES ACIDOPHILIC ACTIVITY.
CONFLICT 111 111 A->R (IN PPF. 3).
SEQUENCE 605 AA; 57667 MW; P16R5CAB122EPB32 CPO64,
Query Match 46.5%, Score 45, DB 1, Length 465,
Best Local Similarity 57.1%, Pred. No. 24;
Matches 9, Conservative 3, Mismatches 3, Indels 0, Gaps 0,
4 IKLEPENPPPYEE 17
:::|:|:|:|:|
105 AIWEPPASPPYEE 119
:::|:|:|:|:|
ULT 14
4_CHLRE STANDARD; PRT; 465 AA.
RSP4_CHLRE
001656;
01-JUN-1993 (Rel. 26, Created)
01-JUN-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Flagellar radial spoke protein 4.
RSP4.
Chlamydomonas reinhardtii; Chlorophyta, Chlorophyceae, Volvocales,
Eukaryota; Viridiplantae; Chlamydomonas,
Chlamydomonadales; Chlamydomonas,
NCBI_TaxID=3006;
[1]
SEQUENCE FROM N.A.
STRAIN-2197,
MEDLINE=9237900; PubMed=1509197;
Curry A M., Williams R D., Rosenbaum D L.;
"Sequence analysis reveals homology between two proteins of the
flagellar radial spoke.";
Mol. Cell Biol. 13:3667-3672(1993).
-1- FUNCTION: FLAGELLAR RADIAL SPOKE CONTRIBUTES TO THE REGULATION
OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING.
THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBFIBER
OF THE OUTER DOUBLE MICROTUBULE, AND A FIBROUS HEAD, WHICH IS
ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE
PROTECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.
-1- SUBUNIT: THE RADIAL SPOKE HEAD IS MADE OF FIVE DIFFERENT
POLYPEPTIDES (RSP1, RSP4, RSP6, RSP9, AND RSP10).
-1- CRYSTALLINE LOCATION: RADIAL SPOKE
-1- SIMILARITY: TO THE FLAGELLAR RADIAL SPOKE PROTEIN 6.
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EMBL: M87526; AAA33092.1; -
PIR: A44498; A44498.
Flagella.
SEQUENCE 465 AA; 47739 MW; A23AFR0307PAB32 CPO64,
Query Match 45.5%, Score 45, DB 1, Length 465,
Best Local Similarity 57.1%, Pred. No. 24;
Matches 9, Conservative 3, Mismatches 3, Indels 0, Gaps 0,
5 IKLEPENPPPYEEA 18
:::|:|:|:|:|
448 IELKPAPPPPEEA 461
:::|:|:|:|:|
LT 15
XENLA STANDARD; PRT; 477 AA.
PPAT_XENLA
P37234;

```

```

DT 01-OCT-1994 (Rel. 30, Created)
RT 01-OCT-1994 (Rel. 30, Last sequence update)
ET 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxisome proliferator activated receptor gamma (PPAR-gamma).
GN PPARG OR NR1C3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia, Pipidae;
OC Xenopodinae, Xenopus.
OX NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=92191207; PubMed=1312391;
RA Dreyer C., Krey G., Keller H., Givel F., Helftenbein G., Wahl W.;
RT "Control of the peroxisomal beta-oxidation pathway by a novel family
of nuclear hormone receptors.";
RL Cell 68:879-887(1992).
[2]
CHARACTERIZATION.
RX MEDLINE=94100165; PubMed=9274443;
PA Krey G., Keller H., Mahfoudi A., Medin J., Ozato K., Dreyer C.,
RA Wahl W.;
RT "Xenopus peroxisome proliferator activated receptors: genomic
organization, response element recognition, heterodimer formation
with retinoid X receptor and activation by fatty acids.";
ET Steroid Biochem. Mol. Biol. 47:65-73(1993).
-1- FUNCTION: RECEPTOR THAT BINDS PEROXISOME PROLIFERATORS SUCH AS
HYDROPHOBIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND,
THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA
OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE
PEROXISOMAL BETA OXIDATION PATHWAY OF FATTY ACIDS. KEY REGULATOR
OF ACTIVATED DIFFERENTIATION AND GLUCOSE HOMEOSTASIS.
-1- SUBUNIT: HETERODIMER WITH THE RETINOID X RECEPTOR.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN ADIPOSE TISSUE AND KIDNEY.
-1- DEVELOPMENTAL STAGE: ADULT.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR1 SUBFAMILY.
CC
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or send an email to license@sib.ch).
CC
CC EMBL: M84163; AAA9937.1, -
DR PIR: C42214; C42214.
DR HSSP: P37231; IFM9.
DR TRANSFAC, T01354, -
DR InterPro; IPP000536; Hormone_rec_1lg.
DR InterPro; IPP001723; Sterhmr_receptor.
DR InterPro; IPP001628; ZnF_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRHDQRMNER.
DR PRINTS; PR00047; STROIDFINGER.
DR PROSITE; PS00035; ZnF_C4steroid; 1.
DR SMART; SM00430; HOLL; 1.
DR SMART, SMC0399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAP_PPRTOP; 1.
KW Receptor; Transcription regulation; Activator; DNA binding;
KW Nuclear protein; zinc-finger, Multigene family, Phosphorylation.
FT DNA_BIND 113 177 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 113 133 C4-TYPE.
FT ZN_FING 150 172 C4-TYPE.
FT DOMAIN 293 477 LIGAND BINDING (POTENTIAL).
FT MOD_PES 87 87 PHOSPHORYLATION (BY MAPK) (BY
SIMILARITY).
SQ SEQUENCE 477 AA; 54055 MW; 160F87A401CE7246 CRC64,
Query Match 45.5%, Score 45, DB 1, Length 477;

```





GenCore version 5.1.3  
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protein - protein search, using sw model

January 24, 2003, 11:09:13, Search time 23 Seconds  
(without alignments)  
127 801 Million cell updates/sec

US-09-893-348-19

Effect score: 99

Sequence: 1 SYDSITMPPNPVPERA 18

Align ratio: PROSWGC

Gapop 10 0, Gapext 0 5

Aligned: 671580 seqs, 206047115 residues

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Minimum PP seq length: 2000000000

Minimum PP seq length: 2000000000

Minimum Match 38

Maximum Match 100%

Listing first 45 summaries

Phase:

SPTREMBL 21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rviro:  
16: sp\_bacterial:  
17: sp\_archaeal:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

ID	Query	Match	Length	PP	10	Description
1	59	59.6	532	13	Q9W712	Q9W712 pleurorecte
2	59	59.6	532	13	Q9W712	Q9W712 pleurorecte
3	51	51.5	2957	5	Q61845	Q61845 caenorhabdi
4	50	50.5	442	2	Q51880	Q51880 phormidium
5	50	50.5	473	10	Q40778	Q40778 parthenium
6	49	49.5	306	5	Q9VAC5	Q9VAC5 drosophila
7	49	49.5	458	16	Q8YT49	Q8YT49 anabaena sp
8	49	49.5	1398	5	Q91099	Q91099 caenorhabdi
9	49	49.5	1398	5	Q91099	Q91099 caenorhabdi
10	48	48.5	158	11	Q9PCT0	Q9PCT0 mus musculus
11	47	47.5	125	4	Q9UES1	Q9UES1 homo sapien
12	47	47.5	157	4	Q76025	Q76025 homo sapien
13	47	47.5	257	17	Q91787	Q91787 fyrococcus
14	47	47.5	275	4	Q9RU77	Q9RU77 homo sapien
15	47	47.5	213	4	Q9W712	Q9W712 homo sapien
16	47	47.5	313	6	Q9SKJ0	Q9SKJ0 macaca fasc

17	47	47.5	313	11	Q9D0D4	Q9D0D4 mus musculus
18	47	47.5	983	5	Q9NE58	Q9NE58 leishmania
19	46.5	47.0	246	16	Q9LIM6	Q9LIM6 streptomyces
20	46	46.5	156	5	Q9XT27	Q9XT27 caenorhabdi
21	46	46.5	186	2	Q9PC83	Q9PC83 bacillus ha
22	46	46.5	189	12	Q92Y74	Q92Y74 bacillus fin
23	46	46.5	191	10	Q9S0M5	Q9S0M5 oryza sativ
24	46	46.5	207	16	Q9CFE7	Q9CFE7 arabidopsis
25	46	46.5	330	16	Q9KCE0	Q9KCE0 bacillus ha
26	46	46.5	340	10	Q9FMU9	Q9FMU9 arabidopsis
27	46	46.5	340	10	Q9LY13	Q9LY13 arabidopsis
28	46	46.5	355	10	Q9CED3	Q9CED3 arabidopsis
29	46	46.5	475	6	Q9SUI7	Q9SUI7 macaca fasc
30	46	46.5	475	11	Q9APC7	Q9APC7 avia puce
31	46	46.5	477	4	Q96012	Q96012 homo sapien
32	46	46.5	477	4	Q96012	Q96012 homo sapien
33	46	46.5	539	5	Q90065	Q90065 caenorhabdi
34	46	46.5	807	5	Q8SSX1	Q8SSX1 dictyosteli
35	46	46.5	1113	5	Q9XXK4	Q9XXK4 caenorhabdi
36	45.5	46.0	308	11	Q91XA6	Q91XA6 mus musculu
37	45.5	46.0	427	13	Q9W712	Q9W712 oryza sativ
38	45	45.5	41	6	Q9GKL3	Q9GKL3 sus scrofa
39	45	45.5	90	12	Q9Y1W6	Q9Y1W6 lymphocytic
40	45	45.5	257	12	Q9Y1W6	Q9Y1W6 simian aden
41	45	45.5	284	10	Q9K256	Q9K256 arabidopsis
42	45	45.5	317	10	Q9K256	Q9K256 arabidopsis
43	45	45.5	317	10	Q9K256	Q9K256 arabidopsis
44	45	45.5	400	16	Q96549	Q96549 streptomyces
45	45	45.5	459	16	Q9KDY2	Q9KDY2 bacillus ha

## ALIGNMENTS

RESULT 1  
ID Q9W712 PRELIMINARY, FRT, 532 AA.  
AC Q9W712;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Peroxisome proliferator-activated receptor gamma.  
GN PPAP.  
OS Pleuronectes plateosa (Plaice).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;  
OC Pleuronectidae; Pleuronectes.  
OX NCBI\_TaxID:8262;  
RN [1]  
PP SEQUENCE FROM N A  
RA Leaver M.J.;  
RT "A peroxisome proliferator-activated receptor gamma gene from a marine fish."  
KL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC 1. SUBCELLULAR LOCATION: NUCLEAR (By similarity).  
CC 2. SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.  
DR EMBL; AJ249075; CAB51396.1; JOINED.  
DR EMBL; AJ249075; CAB51396.1; JOINED.  
DR EMBL; AJ249077; CAB51396.1; JOINED.  
DR EMBL; AJ249078; CAB51396.1; JOINED.  
DR EMBL; AJ249079; CAB51396.1; JOINED.  
DR EMBL; AJ249080; CAB51396.1; JOINED.  
DR HSSP; P37231; 1FM9  
DR InterPro; IPR000536; Hormone\_rec\_1lg.  
DR InterPro; IPR01628; Znf\_C4steroid.  
DR Pfam; PF00104; hormone\_rec; 1.  
DR Pfam; PF00105; zf-C4; 1.  
DR PRINTS; PR00047; STROIDFINGER.  
DR PROSITE; PS00035; Znf\_C4steroid; 1.  
DR SMART; SM00430; HOL1; 1.  
DR SMART; SM00399; Znf\_C4; 1.  
DR PROSITE; PS00011; NUCLEAR\_RECEPTOR; 1.



Thesis (1993), Biochemistry and Molecular Biology,  
University of Basque Country.

[2]

SEQUENCE FROM N A  
STRAIN=OH-1-P-CUI;

Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N A  
STRAIN=OH-1-P-CUI;

MEDLINE=95284340, PubMed-7766873,

Merchan F, Kintle K L, Llana M J, Serra J L, Fernandez E;  
"Isolation, sequence and expression in *Escherichia coli* of the nitrite  
reductase gene from the filamentous, thermophilic cyanobacterium  
*Phormidium laminosum*,"

Plant Mol Biol 27:1037-1042(1995).

[4]

SEQUENCE FROM N A  
STRAIN=OH-1-P-CUI;

Fernandez E;  
Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases

[5]

SEQUENCE FROM N A  
STRAIN=OH-1-P-CUI;

MEDLINE=95375238, PubMed-7647306,  
Merchan F, Kintle K L, Llana M J, Serra J L, Fernandez E;  
"Cloning and sequencing of the nitrate transport system from the  
thermophilic, filamentous cyanobacterium *Phormidium laminosum*:  
comparative analysis with the homologous system fromis with the  
heterologous system from *Synedra racemosa* sp. nov 7942,"

Plant Mol Biol 28:759-766(1995).

EMBL/ Z19598; CAA79656.1;

SEQUENCE 442 AA; 47719 MW; 76A0FD840535EF8 CRC64;

Query Match 50.5%, Score 50, DB 2, Length 442;

Best Local Similarity 47.1%; Pred No 14;

Matches 8, Conservative 3, Mismatches 6, Indels 0, Gaps 0,

2 YDSIKLEPPPPYEEA 18

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

420 FDGVKFDPPNSAYLSA 436

RT allene oxide synthase, resembles that of animal prostaglandin

RT endoperoxide H synthase,"

PL J. Biol. Chem 273:18139-18145(1998)

CC -1- FUNCTION: IS INVOLVED IN THE BIOSYNTHESIS OF JASMONIC ACID, A

CC GROWTH REGULATOR THAT IS IMPLICATED ALSO AS A SIGNALING MOLECULE

CC IN PLANT DEFENSE ACTS ON A NUMBER OF UNSATURATED FATTY-ACID

CC HYDROPEROXIDES, FORMING THE CORRESPONDING ALLENE OXIDES (BY

CC SIMILARITY).

CC -1- CATALYTIC ACTIVITY (32,11E,14Z) (13S) HYDROPEROXYOCTADEC-

CC (9,11,14)-TRIENIC ACID = (9Z)-11Z)-13Z)-14Z)-15Z)-16Z)-17Z)-18Z)-

CC + H(2)O.

CC -1- SUPRACELLULAR LOCATION: PLASMA PARTICLE.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DE EMBL; X78166; CAA55025.1;

DE InterPro; IPR001199; Cytochrome\_P450.

DE Pfam; PF00067; P450; 1.

DE PROSITE; PS00086; CYTOCHROME\_P450; FALSE\_NEG.

DE Lyase; Heme.

FT METAL 426 426 HEME (BY SIMILARITY).

FT CONFLICT 415 415 E -> EE (IN AA SEQUENCE).

SC SEQUENCE 473 AA, 53460 MW, PF371266A0197APF CRC64;

Query Match 50.5%, Score 50, DB 10, Length 473;

Best Local Similarity 47.1%; Pred No 15;

Matches 8, Conservative 5, Mismatches 4, Indels 0, Gaps 0;

2 YDSIKLEPPPPYEEA 18

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

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335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

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335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351

335 YESLRIEPPVPPYQKA 351



Q9USU2; Q9Y7V3;  
01-MAY-2000 (TReMBLrel. 13, Created)  
01-JUN-2002 (TReMBLrel. 13, Last sequence update)  
01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-ADENOSYL(PRNA) dimethyltransferase) (18S RNA dimethylase).  
DIM1 OR SPBC336.02.  
Schizosaccharomyces pombe (Fission yeast).  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomycetes.  
NCBI\_TaxID=4896;  
[1]  
SEQUENCE FROM N.A.  
Housen I., Demonte D., Lafontaine P., Vandenhautte J.,  
"Cloning and comparative analysis of the SPD1M gene from  
Schizosaccharomycetes pombe";  
Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
STRAIN=972;  
Borzum K., Beck A., Reinhardt R., McDougall R.C., Rajandream M.A.,  
Barrell B.G.;  
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
-1- FUNCTION: SPECIFICALLY DIMETHYLATES TWO ADJACENT ADENOSINES IN THE  
LOOP OF A CONSERVED HAIRPIN NEAR THE 3'-END OF 18S RNA IN THE 40S  
PARTICLE.  
-1- SIMILARITY: BELONGS TO THE RNA ADENINE N-6-METHYLTRANSFERASE  
FAMILY.  
EMBL; Z68293; CAA92585.1; -;  
EMBL; AL121815; CAB58154.1; -;  
InterPro; IPR001737; RNA\_A\_dimeth.  
InterPro; IPR000051; SAM\_Bind.  
Pfam; PF00198; RnaAD; 1.  
TIGRFAMS; TIGR00755; ksgA; 1.  
PROSITE; PS01131; RNA\_A\_DIMETH; 1.  
mRNA processing; Transferase; Methyltransferase.  
DOMAIN 208 211  
CONFLICT 170 170 S->P (IN REF. 1).  
CONFLICT 290 292 TEF->QS (IN REF. 1).  
CONFLICT 298 298 A->P (IN REF. 1).  
CONFLICT 304 307 VHFA->RSFWLMGQDGVFH (IN REF. 1).  
SEQUENCE 307 AA; 34678 MW; E2F4543EB190B94A CRC64;  
Query Match  
Best Local Similarity 49.0%; Score 48.5; DB 3; Length 307;  
Matches 8; Conservative 5; Mismatches 0; Indels 3; Gaps 1;  
5 IKLEPENPPP---YEE 17  
:::|||||  
201 VRIEPPKPPPLAFEE 216  
/LT 10  
TO  
Q9DCT0 PRELIMINARY; PRT; 158 AA.  
Q9DCT0; 01-JUN-2001 (TReMBLrel. 17, Created)  
01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
0610010012Pik protein.  
0610010012Pik.  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=KIDNEY;  
MEDLINE=21085660; PubMed=11217851;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Picole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK002512; BAB2153.1; -;  
DR MGD; MGI:1913310; 0610010012Rik.  
SQ SEQUENCE 158 AA; 16764 MW; 9122F577DF49D2B4 CRC64;

Query Match  
Best Local Similarity 48.5%; Score 48; DB 11; Length 158;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 LEPENPPY 15  
:|||||  
Db 1 MNPENPPY 9

RESULT 11  
Q9UES1 PRELIMINARY; PRT; 125 AA.  
AC Q9UES1;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE Hypothetical 14.3 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barrow I.K.-P., Boguski M.S., Touchman J., Spencer F.;  
RT "Full-insert sequence of mapped XREF EST."  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF091078; AAC72947.1; -;  
DR InterPro; IPR001737; RNA\_A\_dimeth.  
DR Pfam; PF00398; RnaAD; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 125 AA; 14275 MW; 9E2E91518577BD01 CRC64;

Query Match  
Best Local Similarity 47.5%; Score 47; DB 4; Length 125;  
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IKLEPENPPP 14  
:::|||||  
Db 19 VRIEPPKPP 28

RESULT 12  
O76025 PRELIMINARY; PRT; 157 AA.  
AC O76025;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE Putative dimethyladenosine transferase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.





GenCore Version 5.1.3  
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Protein - protein search, using SW model

January 24, 2003, 11:09:59 Search time 15 seconds  
(without alignments)  
35.308 Million cell updates/sec

US-09-893-348-19

Test score: 99  
Sequence: 1 SYDSIKLEPPPPYEEA 18

Matrix: BLOSUM62

Gapop 10.0, Gapext 0.5

Aligned: 262574 seqs, 20422922 residues

Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Minimum DB seq length: 2000000000

Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:

1: /cogn2\_6/prodata/1/aa/5A\_COWB.ppt \*  
2: /cogn2\_6/prodata/1/aa/5B\_COWB.ppt \*  
3: /cogn2\_6/prodata/1/aa/5A\_COWB.ppt \*  
4: /cogn2\_6/prodata/1/aa/5B\_COWB.ppt \*  
5: /cogn2\_6/prodata/1/aa/5A\_COWB.ppt \*  
6: /cogn2\_6/prodata/1/aa/5B\_COWB.ppt \*

Fried. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Seq No.	Score	Query Match	Length DB	ID	Description
1	50	50.5	405	4	US-09-537-357-54
2	46	46.5	475	2	US-08-484-200-2
3	46	46.5	475	3	US-08-465-375-2
4	46	46.5	475	4	US-08-764-870-10
5	46	46.5	475	4	US-08-980-115-10
6	46	46.5	475	4	US-09-788-070-2
7	46	46.5	475	4	US-09-134-5570-2
8	46	46.5	475	4	US-09-128-142-2
9	46	46.5	505	4	US-09-128-142-4
10	46	46.5	506	4	US-09-514-247A-6
11	44	44.4	250	2	US-09-861-260-5
12	44	44.4	250	2	US-09-134-596-5
13	44	44.4	250	2	US-09-294-278-5
14	43	43.4	241	2	US-08-379-556A-4
15	43	43.4	247	2	US-08-379-556A-2
16	43	43.4	488	4	US-08-556-977-137
17	43	43.4	488	4	US-09-620-4120-207
18	43	43.4	488	4	US-08-943-768-2
19	42	42.4	293	2	US-08-132-622A-136
20	42	42.4	433	5	US-08-691-814B-8
21	42	42.4	534	2	US-08-691-814B-8
22	42	42.4	913	1	US-08-445-640-4
23	42	42.4	913	3	US-08-170-558-4
24	42	42.4	913	3	US-08-447-314-4
25	42	42.4	913	3	US-08-445-461-4
26	42	42.4	913	3	US-08-338-343A-2
27	41	41.4	26	1	US-08-732-751-8

29	41	41.4	27	1	US-08-732-751-12	Sequence 12, Appl
29	41	41.4	27	2	US-08-236-886-1	Sequence 1, Appl
30	41	41.4	28	1	US-08-732-751-11	Sequence 11, Appl
31	41	41.4	30	1	US-08-732-751-7	Sequence 7, Appl
32	41	41.4	31	1	US-07-596-081A-1	Sequence 1, Appl
33	41	41.4	31	1	US-07-596-081A-24	Sequence 24, Appl
34	41	41.4	33	1	US-07-596-081A-6	Sequence 6, Appl
35	41	41.4	33	2	US-08-146-028-171	Sequence 171, Appl
36	41	41.4	33	2	US-08-146-028-171	Sequence 171, Appl
37	41	41.4	33	4	US-08-723-425A-32	Sequence 32, Appl
38	41	41.4	33	4	US-08-723-425A-171	Sequence 171, Appl
39	41	41.4	33	4	US-09-112-206-12	Sequence 12, Appl
40	41	41.4	33	4	US-09-112-206-171	Sequence 171, Appl
41	41	41.4	45	3	US-08-236-886-2	Sequence 2, Appl
42	41	41.4	254	4	US-08-362-831-3	Sequence 3, Appl
43	41	41.4	429	1	US-07-672-493-2	Sequence 3, Appl
44	41	41.4	429	4	US-09-370-368-6	Sequence 6, Appl
45	41	41.4	429	6	5182105-13	Patent No. 5182195

#### ALIGNMENTS

RESULT 1  
US-09-537-357-54  
Patent No. 6271018  
GENERAL INFORMATION:  
APPLICANT: Alan Brash  
TITLE OF INVENTION: MUSPERION (CUTTING VEIN) HYPERPROTECTIVE  
FILE REFERENCE: 00027 0002  
CURRENT APPLICATION NUMBER: US/09/537,357  
CURRENT FILING DATE: 2000-09-23  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Guayule  
US-09-537-357-54

Query Match 50.5%; Score 50; FR 4; Length 405;  
Post local Similarity 47.1%; Fried No 6.5;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

CY 2 SYDSIKLEPPPPYEEA 18  
nb 180 YFSIRPPPPVPPQYCKA 196

RESULT 2  
US-09-537-357-54  
Patent No. 5861274  
GENERAL INFORMATION:  
APPLICANT: EVANS, RONALD M.  
APPLICANT: POPMAN, RABBY M.  
APPLICANT: KLEWER, STEVEN A.  
TITLE OF INVENTION: HAVEL MEMBERS OF THE STEREOISOMEROID  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSER: PRETTY, SCHROEDER, PRINGSMANN & CLARK  
STREET: 444 SOUTH FLOWER STREET, SUITE 2000  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/404,200  
FILING DATE: 07 JUN 1995  
CLASSIFICATION:

ACTOR/RENT/AGENCY INFORMATION.  
NAME: REITER, STEPHEN E.  
REGISTRATION NUMBER: 31,192  
FEE/REG: 1000.00, REG. NUMBER: 601 3721  
TELECOMMUNICATION INFORMATION.

INFORMATION FOR SEQ ID NO: 2

SEQUENCE CHARACTERISTICS:

LENGTH: 475 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

4 494 200 2

Library Match	46.5%	Score 46,	EB 2,	Length 470,
First Local Similarity	47.1%	Pred. No. 30;		
Clashes	4;	Conservative	3;	Mismatches
				Indels

4 MLEHPYEE 17  
: : : : :  
75 AKVETASTPYEE 88

Parcels 2, Application No. 6022897

INVENTOR: JEFFREY A. EVANS, Ronald M.  
APPLICANT: Evans, Barry M.  
TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME  
CYTOLE OF INVENTION: PROLIFERATOR ACTIVATED RECEPTOR- $\beta$ -GALNA, AND METHODS FOR THE  
TITLE OF INVENTION: USE THEREOF  
CITE REFERENCE: SAKIMURA70-1  
CURRENT APPLICATION NUMBER: US/08/465,375A  
CURRENT FILING DATE: 1995-06-05  
EARLIER APPLICATION NUMBER: 08/428,559  
EARLIER FILING DATE: 1995-04-25  
NUMBER OF SEQ ID NO.: 7  
SOFTWARE: Fast SEQ for Windows Version 4.0

Story Match	46.58%	Score 467	DB 37	Length 475
Post Local Similarity	57.18%	Pred. No. 307		
Verbosity	3	Misclassification	3	Index

4. SIKKEPENNIPYCE 17  
: : : : :  
5. AKVHASTYXCH 08

Page 4  
08/64 870 10  
Page 10, Application US/08764870  
Agent No. 626946

APPLICANT: Schriber, Thomas S.  
 APPLICANT: Raper, John D.  
 APPLICANT: Fletcher, Robert J.  
 APPLICANT: Warner, Richard L.  
 APPLICANT: Kasper, Peter J.

```

APPLICANT: Apriletti, James W
APPLICANT: West, Brian
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
TITLE OF INVENTION: Binding Domains
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1 0, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/AGENT NUMBER: 00741 241 100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 843-5000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-764-870-10

Query Match 46.5%; Score 46; DB 4; Length 475;
Best Local Similarity 57.1%, Pred. No. 30,
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPENPPPYEE 17
:|:|:|:|:|:|
Db 75 AIKEVPASPPYSE 88

RESULT 5
US-08-980-115-10
Sequence ID, Application US/08980115
Patent No. 6266622
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Fletcher, Robert J
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiao, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS
FILE REFERENCE: USAL-246/020US
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
EARLIER FILING DATE: 1996-12-13

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QY	4	SIKLEPENPPYEE	17
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Db	75	AIKVEPASPYYSE	88

RESULT 5  
US-08-980-115-10

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sequence ID: Application US/06380115
Patent No. 6266622
GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Fletcher, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: West, Brian L.
APPLICANT: Shiao, Andrew K.
TITLE OF INVENTION: MULTISAR RECEIVER LOCATES AND LOGS EMIING COORDIN
FILE REFERENCE: USAL-246/020US
CURRENT APPLICATION NUMBER: US/02/380,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,970
EARLIER FILING DATE: 1996-12-13

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EARLIER APPLICATION NUMBER: 60/008,606  
EARLIER FILING DATE: 1995-12-14  
EARLIER APPLICATION NUMBER: 60/008,543  
EARLIER FILING DATE: 1995-12-13  
EARLIER APPLICATION NUMBER: 60/008,540  
EARLIER FILING DATE: 1995-12-13  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patent In Ver 2.0  
SEQ ID NO 10  
LENGTH: 475  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (202) (475)  
OTHER INFORMATION: minimal ligand binding domain  
-08-940-115-10

Query Match 46.5%; Score 46; DR 4; Length 475;  
Best Local Similarity: 57.1%; Pred. No. 30;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0,  
4 SIKLEPENPPYEE 17  
:|||||:  
75 AIKVEPASPYYSE 88

SUBT 6  
Sequence 2, Application US/09798070  
Patent No. 6413994  
GENERAL INFORMATION:  
APPLICANT: EVANS, RONALD  
APPLICANT: FORMAN, BARRY  
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA,  
FILE REFERENCE: SALK1480.2  
CURRENT AFFILIATION NUMBER: US/09/778A, 070  
CURRENT FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 09/055,302  
PRIOR FILING DATE: 1993-12-22  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent In version 2.0  
SEQ ID NO 2  
LENGTH: 475  
TYPE: PRT  
ORGANISM: Mus musculus  
09-788-070-2

Query Match 46.5%; Score 46; DR 4; Length 475;  
Best Local Similarity: 57.1%; Pred. No. 30;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
4 SIKLEPENPPYEE 17  
:|||||:  
75 AIKVEPASPYYSE 88

SUBT 7  
Sequence 2, Application US/0913457D  
Patent No. 6000903  
GENERAL INFORMATION:  
APPLICANT: Greene, Marianne R.  
APPLICANT: Blumberg, Bruce  
TITLE OF INVENTION: Human Peroxisome Proliferator Activated  
RECEPTOR GAMMA: Compositions and Methods  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pockey, Milmarow & Katz, Ltd.  
STREET: 2 Prudential Plaza, Suite 4700 180 N. Stetson  
CITY: Chicago  
STATE: IL

COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/134,557D  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Katz, Martin L.  
REGISTRATION NUMBER: 25,011  
REFERENCE/DOCKET NUMBER: APOH:098  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS  
LENGTH: 476 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-134-557D-2

Query Match 46.5%; Score 46; DR 4; Length 476;  
Best Local Similarity: 57.1%; Pred. No. 30;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 4 SIKLEPENPPYEE 17  
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DB 75 AIKVEPASPYYSE 88

RESULT 8  
US-09-128-142-2  
Sequence 2, Application US/09109142  
Patent No. 6294559  
GENERAL INFORMATION:  
APPLICANT: Smith, Roy G.  
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH  
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS GAMMA1 AND GAMMA2  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jack L. Tribble  
STREET: 126 F. Lincoln Ave., P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Power Macintosh 7500/100  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,142  
FILING DATE: 03-Aug-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/344,007  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO. 2.

Query Match 46.5% Score 46; DB 4; Length 477;  
Best Local Similarity 57.1% Freq. No. 32;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPNPYYE 17  
|||||  
77 AIKVEPASPYYSE 90

DEF 9  
9-128 142 4  
Reference 4; Application US/09128142  
Patent No. 6294559  
GENERAL INFORMATION:

APPLICANT: Smith, Roy G.  
TITLE OF INVENTION: ANTIPROLIFERATIVE AGENTS ASSOCIATED WITH  
PEROXISOME PROLIFERATOR ACTIVATED RECEPTORS (PAMPA) AND GAMA

NUMBER OF SEQUENCES: 4  
ADDRESS/ADDRESS: 4  
ADDRESS: Jack L. Tibble  
STREET: 126 E. Lincoln Ave., P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: US  
ZIP: 07065 0907

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Power Macintosh 7500/100  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/128,142  
FILING DATE: 03 Aug 1998  
CLASSIFICATION: <Unknown>

Prior APPLICATION DATA:  
APPLICATION NUMBER: 08/844,007  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Tibble, Jack L.  
REGISTRATION NUMBER: 12,633  
REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 505 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO. 4.

9-128 142 4

Query Match 46.5% Score 46; DB 4; Length 505;  
Best Local Similarity 57.1% Freq. No. 32;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPPNPYYE 17  
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105 AIKVEPASPYYSE 118

DEF 10  
9-514 247A 6  
Reference 6; Application US/0914247A

Patent No. 6365361  
GENERAL INFORMATION:  
APPLICANT: TANABE SEIYAKU CO. LTD.  
APPLICANT: TANIGUCHI, Tomoyasu  
APPLICANT: MIZUKAMI, Junko  
TITLE OF INVENTION: METHOD FOR IDENTIFYING OF SCREENING AGENT AND ANTAGONIST TO PPA  
FILE REFERENCE: TANIGUCHI=6  
CURRENT APPLICATION NUMBER: US/09/514,247A  
CURRENT FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: EP/09/03734  
PRIOR FILING DATE: 1998-08-24  
PRIOR APPLICATION NUMBER: EP231084/1997  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 6  
LENGTH: 506  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-514-247A-6

Query Match 46.5% Score 46; DB 4; Length 506;  
Best Local Similarity 57.1% Freq. No. 32;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPPNPYYE 17  
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Db 105 AIKVEPASPYYSE 118

RESULT 11  
US-08-861-269-5  
Sequence 5; Application US/08861269  
Patent No. 5817494

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Corley, Neil C.  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purni  
TITLE OF INVENTION: TRYPHOSIN CONJUGATION PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/861,269  
FILING DATE: Filed Herewith  
Prior APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0302 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:



LIBRARY: 397581  
CLONE: GenBank  
09-861-269-5

Query Match 44.4% Score 44, DB 2, Length 250,  
Best Local Similarity 80.0%, Pred. No. 30,  
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

6 KLEPENPPY 15  
|||  
15 KLMVENPPY 24

RESULT 12  
09-134-596-5  
Sequence 5, Application US/09134596  
Patent No. 5922319

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Corley, Neil C.  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,273  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/134,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0302 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: 397581  
CLONE: GenBank  
09-134-596-5

Query Match 44.4% Score 44, DB 2, Length 250,  
Best Local Similarity 80.0%, Pred. No. 30,  
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

6 KLEPENPPY 15  
|||  
15 KLMVENPPY 24

RESULT 13  
09-293-273-5  
Sequence 5, Application US/09293273  
Patent No. 6003112

GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Corley, Neil C.  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: UBIQUITIN CONJUGATION PROTEINS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/293,273  
FILING DATE:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/134,596  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0302 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 250 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: 397581  
CLONE: GenBank  
US-09-293-273-5

Query Match 44.4% Score 44, DB 3, Length 250,  
Best Local Similarity 80.0%, Pred. No. 30,  
Matches 8, Conservative 0, Mismatches 2, Indels 0, Gaps 0

QY 6 KLEPENPPY 15  
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DB 15 KLMVENPPY 24

RESULT 14  
US-08-379-556A-4  
Sequence 4, Application US/08379556A  
Patent No. 5859329

GENERAL INFORMATION:  
APPLICANT: HOLTON, TIMOTHY A.  
APPLICANT: KEAM, LISA A.  
TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOL  
TITLE OF INVENTION: SYNTHASE ENZYMEs AND USES THEREFORE  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER  
STREET: 400 GARDEN CITY PLAZA  
CITY: GARDEN CITY  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

Protein Protein search, using sw model

January 24, 2003, 11:10.33 , Search time 10 Seconds  
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US-09-893-348-19  
Effect score: 99  
Sequence: 1 SYDSIKLEPPENPPYEBA 18

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Maximum Match 100%  
Listing first 45 summaries

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Alt	Score	Query Match	Length	DB	ID	Description
1	99	100.0	18	10	US-09-893-348-19	Sequence 19, Appl
2	99	100.0	1163	10	US-09-893-348-18	Sequence 18, Appl
3	85	85.9	1192	10	US-09-789-386-2	Sequence 2, Appl
4	85	85.9	1192	10	US-09-758-140-6	Sequence 6, Appl
5	85	85.9	1192	10	US-09-893-348-23	Sequence 23, Appl
6	85	85.9	1192	10	US-09-972-599A-6	Sequence 6, Appl
7	50	50.5	405	10	US-09-884-260A-54	Sequence 54, Appl
8	46	46.5	475	12	US-10-142-373-2	Sequence 2, Appl
9	46	46.5	478	10	US-09-765-111A-27	Sequence 27, Appl
10	46	46.5	505	10	US-09-765-111A-16	Sequence 16, Appl
11	46	46.5	506	12	US-10-109-886-6	Sequence 6, Appl
12	46	46.5	688	9	US-09-931-007A-1	Sequence 1, Appl
13	46	46.5	777	10	US-09-765-111A-2	Sequence 2, Appl
14	46	46.5	811	10	US-09-765-111A-23	Sequence 23, Appl
15	46	46.5	840	10	US-09-765-111A-4	Sequence 4, Appl
16	46	46.5	874	10	US-09-765-111A-6	Sequence 6, Appl
17	45	45.5	158	10	US-09-864-761-39748	Sequence 39748, A
18	43	43.4	488	10	US-09-841-132-297	Sequence 297, App
19	43	43.4	609	10	US-09-841-132-431	Sequence 431, App

20	43	43.4	789	9	US-09-712-363-244	Sequence 244, App
21	43	43.4	912	9	US-09-865-960-2	Sequence 2, Appl
22	43	43.4	928	10	US-09-993-170-58	Sequence 58, Appl
23	42	42.4	73	9	US-10-001-887-94	Sequence 94, Appl
24	42	42.4	624	10	US-09-925-297-738	Sequence 738, App
25	42	42.4	913	10	US-09-223-490-4	Sequence 4, Appl
26	41	41.4	128	10	US-09-925-239-882	Sequence 882, App
27	41	41.4	429	10	US-09-827-822-6	Sequence 6, Appl
28	40.5	40.9	2665	10	US-09-864-761-34248	Sequence 34248, A
29	40	40.4	311	10	US-09-908-670-1	Sequence 1, Appl
30	40	40.4	313	10	US-09-925-302-666	Sequence 666, App
31	40	40.4	684	10	US-09-765-298A-18	Sequence 18, Appl
32	40	40.4	731	9	US-10-086-464-8	Sequence 8, Appl
33	39.5	39.9	402	10	US-09-925-301-984	Sequence 984, App
34	39	39.4	59	10	US-09-764-877-1169	Sequence 1169, App
35	39	39.4	63	10	US-09-864-761-36982	Sequence 36982, A
36	39	39.4	99	10	US-09-925-300-1634	Sequence 1634, App
37	39	39.4	119	9	US-09-852-209A-24	Sequence 24, Appl
38	39	39.4	119	9	US-10-086-623-24	Sequence 24, Appl
39	39	39.4	146	9	US-10-174-590-376	Sequence 376, App
40	39	39.4	146	9	US-10-176-758-376	Sequence 376, App
41	39	39.4	146	9	US-10-175-737-376	Sequence 376, App
42	39	39.4	146	12	US-10-052-586-375	Sequence 376, App
43	39	39.4	200	9	US-10-107-868-16	Sequence 16, Appl
44	39	39.4	200	12	US-10-107-829-16	Sequence 16, Appl
45	39	39.4	200	12	US-10-107-907-16	Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-893-348-19  
Sequence 19, Application US/09893348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michal  
APPLICANT: COHEN, Irun R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONIGO, Alon  
APPLICANT: MOALEM, Gil  
TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES  
FILE REFERENCE: EIS-SCHWARTZ-2A  
CURRENT APPLICATION NUMBER: US/09/893,348  
PRIOR FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/314,161  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: US 09/218,277  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 19  
LENGTH: 18  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-893-348-19

Query Match 100.0%; Score 99; DB 10; Length 18;  
Best local similarity 100.0%; Pred. No. 3.4e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYDSIKLEPPENPPYEBA 18  
Db 1 SYDSIKLEPPENPPYEBA 18

RESULT 2  
US-09-893-348-18  
Sequence 18, Application US/09893348

Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michael  
APPLICANT: COHEN, Irum R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONIGO, Alon  
APPLICANT: MOALEM, Gila  
TITLE OF INVENTION: ACTIVATED T CELLS, NERVOUS SYSTEM SPECIFIC ANTIGENS AND THEIR USE  
FILE REFERENCE: EIS-SCHWARTZ=2A  
CURRENT FILING DATE: 2001-06-28  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: US 09/214,161  
PRIOR FILING DATE: 1998-07-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 18  
LENGTH: 1163  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
Query Match: 100.0%; Score 89; DB 10; Length 1163;  
Best Local Similarity: 100.0%; Pred. No. 2,9e-06;  
Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
1 SYDSIKLEPPENPPYEAA 18  
:|||||  
623 SYDSIKLEPPENPPYEAA 649  
SEQUENCE 2, Application US/0772386  
Patent No. US20020010324A1  
GENERAL INFORMATION:  
APPLICANT: MICHAJOVICH, DAVID  
APPLICANT: PRINJHA, RAHINDER KUMAR  
TITLE OF INVENTION: NOVEL COMPOUNDS  
FILE REFERENCE: CP-10165-C1  
CURRENT APPLICATION NUMBER: US/09/789,386  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: U.K. 9916808 1  
PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: U.K. 9816024.5  
PRIOR FILING DATE: 1998-07-22  
PRIOR APPLICATION NUMBER: US 09/359,208  
PRIOR FILING DATE: 1999-07-22  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
Query Match: 85.9%; Score 85; DB 10; Length 1192;  
Best Local Similarity: 83.3%; Pred. No. 0.00027;  
Matches: 15; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;  
1 SYDSIKLEPPENPPYEAA 18  
:|||||  
645 NYESIKHEPPENPPYEAA 662  
SEQUENCE 4  
US-09-758-140-6  
Sequence 6, Application US/077259A1

Patent No. US20020012965A1  
GENERAL INFORMATION:  
APPLICANT: Stittmatter, Stephen M.  
TITLE OF INVENTION: NS-1570201-7965A1 Growth  
FILE REFERENCE: 44574-5073-US  
CURRENT APPLICATION NUMBER: US/09/759,140  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: US 60/175,707  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: US 60/277,366  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 60/236,378  
PRIOR FILING DATE: 2000-09-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-758-140-6  
Query Match: 85.9%; Score 85; DB 10; Length 1192;  
Best Local Similarity: 83.3%; Pred. No. 0.00027;  
Matches: 15; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;  
QY 1 SYDSIKLEPPENPPYEAA 18  
:|||||  
DB 645 NYESIKHEPPENPPYEAA 662  
RESULT 5  
US-09-893-348-23  
Sequence 23, Application US/0989348  
Patent No. US20020072493A1  
GENERAL INFORMATION:  
APPLICANT: EISENBACH-SCHWARTZ, Michael  
APPLICANT: COHEN, Irum R.  
APPLICANT: BESERMAN, Pierre  
APPLICANT: MOSONIGO, Alon  
APPLICANT: MOALEM, Gila  
TITLE OF INVENTION: ACTIVATED T CELLS, NERVOUS SYSTEM SPECIFIC ANTIGENS AND THEIR USE  
FILE REFERENCE: EIS-SCHWARTZ=2A  
CURRENT APPLICATION NUMBER: US/09/893,348  
CURRENT FILING DATE: 2001-06-28  
PRIOR APPLICATION NUMBER: US 09/314,161  
PRIOR FILING DATE: 1999-05-19  
PRIOR APPLICATION NUMBER: US 09/218,277  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: PCT/US98/14715  
PRIOR FILING DATE: 1998-07-21  
PRIOR APPLICATION NUMBER: IL 124500  
PRIOR FILING DATE: 1998-05-19  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 23  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-893-348-23  
Query Match: 85.9%; Score 85; DB 10; Length 1192;  
Best Local Similarity: 83.3%; Pred. No. 0.00027;  
Matches: 15; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;  
QY 1 SYDSIKLEPPENPPYEAA 18  
:|||||  
DB 645 NYESIKHEPPENPPYEAA 662  
RESULT 6  
US-09-972-599A-6  
Sequence 6, Application US/09972599A  
Patent No. US20020072295A1

GENERAL INFORMATION:  
APPLICANT: STRITTMATER, STEPHEN M.  
TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
FILE REFERENCE: C077 CIP US  
CURRENT APPLICATION NUMBER: US/09/472,549A  
CURRENT FILING DATE: 2001-10-06  
PRIOR APPLICATION NUMBER: PCT/US01/01041  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/758,140  
PRIOR FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 60/236,379  
PRIOR FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: 60/207,366  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/175,707  
PRIOR FILING DATE: 2000-01-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1192  
TYPE: PRT  
ORGANISM: Homo sapiens  
09-972-599A-6

Query Match 85.9%; Score 85; DB 10; Length 1192;  
Best Local Similarity 83.3%; Pred. No. 0.00027;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0,

1 SYDSIKLEPPPPYEEA 19  
:|||||  
645 NYDSIKLEPPPPYEEA 602

ULT 7  
09-884-260A-54  
Patent No. US20020004570A1  
GENERAL INFORMATION:  
APPLICANT: Alan Brash  
TITLE OF INVENTION: METHOD FOR DETECTING HIV-1 INFECTION  
TITLE OF INVENTION: LYSASE AND USES THEREOF  
FILE REFERENCE: 06027 000202  
CURRENT APPLICATION NUMBER: US/03/984,260A  
CURRENT FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: 09/537,357  
PRIOR FILING DATE: 2000-03-29  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 54  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Guayule  
09-884-260A-54

Query Match 50.5%; Score 50; DB 10; Length 405;  
Best Local Similarity 47.1%; Pred. No. 6.5;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

2 YDSIKLEPPPPYEEA 18  
:|||||  
180 YFSLPIFPVPPQYGYKA 196

ULT 8  
00-142-373-2  
Sequence 2, Application US/10142373  
Patent No. US20020137665A1  
GENERAL INFORMATION:  
APPLICANT: EVANS, RONALD  
APPLICANT: EOPMAN, BARRY  
TITLE OF INVENTION: MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED  
TITLE OF INVENTION: PROCEPT GAMMA,

TITLE OF INVENTION: AND METHODS FOR THE USE THEREOF  
FILE REFERENCE: SALK1480-2  
CURRENT APPLICATION NUMBER: US/10/142,373  
CURRENT FILING DATE: 2002-05-08  
PRIOR APPLICATION NUMBER: US/09/788,070  
PRIOR FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 09/455,102  
PRIOR FILING DATE: 1999-02-22  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 475  
TYPE: PRT  
ORGANISM: Mus Musculus  
US 10 142 373-2

Query Match 46.5%; Score 46; DB 12; Length 475;  
Best Local Similarity 57.1%; Pred. No. 28;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPPPPYEE 17  
:|||||  
Db 75 AIKVEPASPYYSE 88

RESULT 9  
US-09-765-111A-27  
Sequence 27, Application US/09765111A  
Patent No. US20020106796A1  
GENERAL INFORMATION:  
APPLICANT: Fletcher, Jonathan A.  
TITLE OF INVENTION: FAX8-PFARGamma NUCLEIC ACID MOLECULES  
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF  
FILE REFERENCE: B0801/7196/ERP/MAT  
CURRENT APPLICATION NUMBER: US/09/765,111A  
CURRENT FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/177,109  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/225,079  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27  
LENGTH: 478  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-765-111A-27

Query Match 46.5%; Score 46; DB 10; Length 478;  
Best Local Similarity 57.1%; Pred. No. 28;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPPPPYEE 17  
:|||||  
Db 77 AIKVEPASPYYSE 90

RESULT 10  
US-09-765-111A-16  
Sequence 16, Application US/09765111A  
Patent No. US20020106796A1  
GENERAL INFORMATION:  
APPLICANT: Fletcher, Jonathan A.  
APPLICANT: Kroil, Todd G.  
TITLE OF INVENTION: FAX8-PFARGamma NUCLEIC ACID MOLECULES  
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF  
FILE REFERENCE: B0801/7196/ERP/MAT  
CURRENT APPLICATION NUMBER: US/09/765,111A  
CURRENT FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/177,109  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/225,079



PRIOR FILING DATE: 2000-08-14  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 16  
LENGTH: 505  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-765-111A-16

Query Match 46.5%; Score 46; DB 10; Length 505;  
Best Local Similarity 57.1%; Pred. No. 30;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPENPPYYE 17  
:|||:|||||  
105 AIKVEPASPYYSE 118

FIG 11  
US-109-886-6  
Sequence 6, Application US/10109886  
Patent No. US20020119499A1  
GENERAL INFORMATION:  
APPLICANT: TANABE SEIYAKU CO. LTD.  
APPLICANT: TANIGUCHI, Tomoyasu  
APPLICANT: MIYAKAMI, Junko  
TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND  
ANTAGONIST TO PPAR  
FILE REFERENCE: TANIGUCHI=6  
CURRENT APPLICATION NUMBER: US/10109886  
CURRENT FILING DATE: 2002-04-01  
PRIOR APPLICATION NUMBER: 09/514,247  
PRIOR FILING DATE: 2000-02-28  
PRIOR APPLICATION NUMBER: PCT/JP98/03774  
PRIOR FILING DATE: 1998-08-24  
PRIOR APPLICATION NUMBER: JP231084/1997  
PRIOR FILING DATE: 1997-08-27  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 6  
LENGTH: 506  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-109-886-6

Query Match 46.5%; Score 46; DB 12; Length 506;  
Best Local Similarity 57.1%; Pred. No. 30;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPENPPYYE 17  
:|||:|||||  
105 AIKVEPASPYYSE 118

FIG 12  
US-931-007A-1  
Sequence 1, Application US/09931007A  
Patent No. US20020166132A1  
GENERAL INFORMATION:  
APPLICANT: Aventis Pharma S.A.  
TITLE OF INVENTION: TETRA- $\beta$ -HYDROXY- $\gamma$ -BUTYROLACTONE IN VIVO THE EXPRESSION OF A TRANSGENE BY  
TITLE OF INVENTION: CONDITIONAL INHIBITION  
FILE REFERENCE: 03806.0512  
CURRENT APPLICATION NUMBER: US/09/931,007A  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: FR 00/10730  
PRIOR FILING DATE: 2000-08-18  
PRIOR APPLICATION NUMBER: 00/10730  
PRIOR FILING DATE: 2000-10-11  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 1  
LENGTH: 698

TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc  
LOCATION: (1)..(688)  
OTHER INFORMATION: Sequence for PPAR-gamma-2-gamma-2, a modified human PPAR-gamma (P  
OTHER INFORMATION: epsilon Proliferator Activated Receptor gamma)  
US-09-931-007A-1

Query Match 45.5%; Score 46; DB 3; Length 688;  
Best Local Similarity 57.1%; Pred. No. 41;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPENPPYYE 17  
:|||:|||||  
Db 105 AIKVEPASPYYSE 118

RESULT 13  
US-09-765-111A-2  
Sequence 2, Application US/09765111A  
Patent No. US20020106796A1  
GENERAL INFORMATION:  
APPLICANT: Fletcher, Jonathan A.  
APPLICANT: Kroll, Todd G.  
TITLE OF INVENTION: FAX8 FFAAGamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF  
FILE REFERENCE: B0801/7196/ERP/MAT  
CURRENT APPLICATION NUMBER: US/09/765,111A  
CURRENT FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/177,109  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/225,079  
PRIOR FILING DATE: 2000-09-14  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 777  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-09-765-111A-2

Query Match 46.5%; Score 46; DB 10; Length 777;  
Best Local Similarity 57.1%; Pred. No. 47;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 SIKLEPENPPYYE 17  
:|||:|||||  
Db 377 AIKVEPASPYYSE 390

RESULT 14  
US-09-765-111A-23  
Sequence 23, Application US/09765111A  
Patent No. US20020106796A1  
GENERAL INFORMATION:  
APPLICANT: Fletcher, Jonathan A.  
APPLICANT: Kroll, Todd G.  
TITLE OF INVENTION: FAX8 FFAAGamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF  
FILE REFERENCE: B0801/7196/ERP/MAT  
CURRENT APPLICATION NUMBER: US/09/765,111A  
CURRENT FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: US 60/177,109  
PRIOR FILING DATE: 2000-01-20  
PRIOR APPLICATION NUMBER: US 60/225,079  
PRIOR FILING DATE: 2000-08-14  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 811  
TYPE: PRT  
ORGANISM: Homo Sapiens

09-765-111A-23

## Query Match

Best Local Similarity 46.5%; Score 46; DB 10; Length 811;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPENPPYEE 17

:||||:|||||  
411 AIKVEDPASPYYSE 424

ULT 15

09-765-111A-4

Sequence 4, Application US/09765111A  
Patent No. US20020106796A1

## GENERAL INFORMATION:

APPLICANT: Fletcher, Jonathan A.

APPLICANT: Kroll, Todd G.

TITLE OF INVENTION: PAXA-PPAPGAMA NUCLEIC ACID MOLECULES  
TITLE OF INVENTION: AND POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: B0801/7196/ERP/MAT

CURRENT APPLICATION NUMBER: US/09/765,111A

CURRENT FILING DATE: 2001-01-18

PRIOR APPLICATION NUMBER: US 60/177,109

PRIOR FILING DATE: 2000-01-20

PRIOR APPLICATION NUMBER: US 60/225,079

PRIOR FILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

LENGTH: 840

TYPE: PRT

ORGANISM: Homo Sapiens

09-765-111A-4

## Query Match

Best Local Similarity 46.5%; Score 46; DB 10; Length 840;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

4 SIKLEPENPPYEE 17

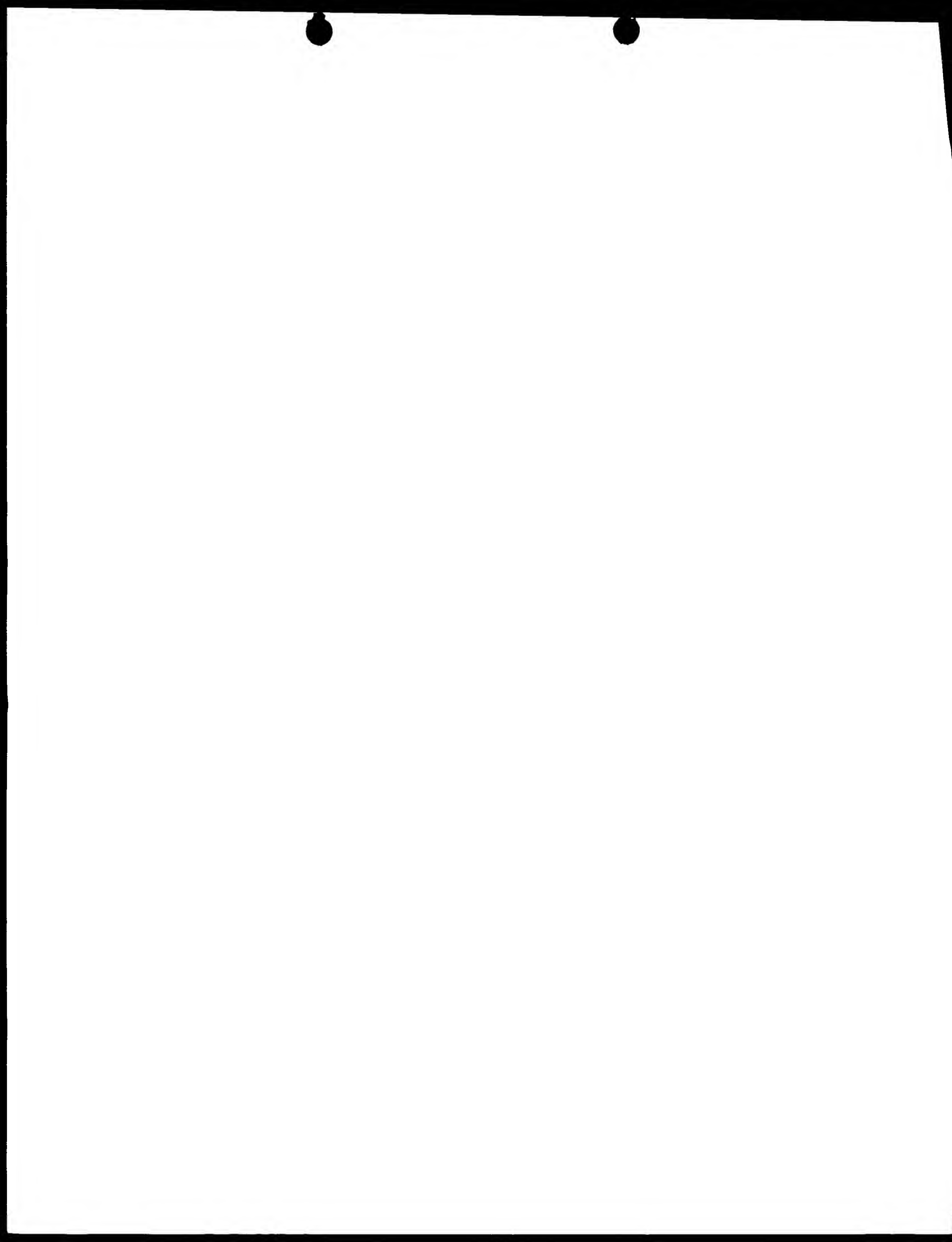
:||||:|||||  
440 AIKVEDPASPYYSE 453Job completed: January 24, 2003, 11:12:28  
Time: 11 secs



Set	Items	Description
S1	2483	NOGO
S2	143.	S1 AND NEUR?
S3	2141	S1 AND NERV?
S4	514	S1 AND CENTRAL(W)NERVOUS(W)SYSTEM
S5	361	ED (unique items)
S6	4.	S5 AND SPINAL(W)CORD
S7		AU='EISENBACH-SCHWARTZ MICHAL'
S8		AU='HAUBEN, EHUD'
S9		AU='HAUBEN, E.'
S10	9.	AU='HAUBEN E'
S11	1.	AU='HAUBEN EHUL'
S12	5.	AU='HAUBEN E.'
S13	14	AU='COHEN, IRUN R'
S14	11.	AU='COHEN IRUN R'
S15	80.	AU='COHEN I E.'
S16	36.	AU='COHEN I.E.'
S17		AU='BESERMAN PIERRE'
S18	4.	AU='MOALEM G'
S19	2.	AU='MOALEM G.'
S20	1.	AU='MOALEM GILA'
S21		AU='MOALEM, GILA'
S22		NOGO AND S7 OR S8 OR S9 OR S10 OR S11 OR S12 OR S13 OR S14 OR S15 OR S16 OR S17 OR S18 OR S19 OR S20 OR S21)
S23	1	ED (unique items)
S24	46	NOGO AND SPINAL(W)CORD
S25	35.	ED (unique items)
S26	16	S25 AND DEGENEFAT?
S27	66	S25 AND REGENEFAT?
?		

09/893,348

DIALOG  
file biosci  
1/24/2003





	Type	Hits	Search Text	DBs
1	BRS	14	EISENBACH-SCHWARTZ-M	USPAT; US-PGPUB; EPO; JPO; DERWENT
2	BRS	16	EISENBACH-SCHWARTZ-MICHAL	USPAT; US-PGPUB; EPO; JPO; DERWENT
3	BRS	3	HAUBEN-EHUD	USPAT; US-PGPUB; EPO; JPO; DERWENT
4	BRS	55	COHEN-IRUN-R	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	BRS	5	BESERMAN-PIERRE	USPAT; US-PGPUB; EPO; JPO; DERWENT
6	BRS	12	BESERMAN	USPAT; US-PGPUB; EPO; JPO; DERWENT
7	BRS	2	MOSONEGO-ALON	USPAT; US-PGPUB; EPO; JPO; DERWENT
8	BRS	2	MOALEM-GILA	USPAT; US-PGPUB; EPO; JPO; DERWENT
9	BRS	266	Nogo	USPAT; US-PGPUB; EPO; JPO; DERWENT
10	BRS	9	Nogo and neuro\$	USPAT; US-PGPUB; EPO; JPO; DERWENT
11	BRS	12	p472	USPAT; US-PGPUB; EPO; JPO; DERWENT
12	BRS	10	Nogo and central adj nervous adj system	USPAT; US-PGPUB; EPO; JPO; DERWENT
13	BRS	6	nogo and spinal adj cord	USPAT; US-PGPUB; EPO; JPO; DERWENT

09/893,348

